IEDB Tools

BRC Meeting

February 6, 2006

IMMUNE EPITOPE DATABASE
AND ANALYSIS RESOURCE

Outline

- Tool integration
- T cell epitope identification tools
- B cell epitope identification tools
- Epitope analysis tools
- Visualization tools

Immune Epitope Database and Analysis Resource - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

Display Settings:	Options:	Analyze Selected Records:
Format: Summary	[New Query]	Tool: T Cell Epitope Prediction
Show: 10	[Revise Query]	Analyze
	[Save Query]	
	[View Query Details]	
	[Define Custom Report]	

9 items found, displaying all items.
Page **1**

	Links	Reference	Structure	Source	Assay
☐	Details	Samita S Andreansky Journal of virology. 2005	RTFSFQLI	Influenza A virus (A/PR/8/34(H1N1)) NS2	T + Cytokine Release-IFN-g
☐	Details	Samita S Andreansky Journal of virology. 2005	LSLRNPILV	Influenza A virus (A/PR/8/34(H1N1)) PB1-F2	T + Cytokine Release-IFN-g
☐	Details	David H Canaday Journal of immunological methods. 2003	GLKGGPSTE	Influenza A virus (A/PR/8/34(H1N1)) Matrix protein 2	T + Cytokine Release-IFN-g
☐	Details	S M Mansour Haeryfar Journal of immunology (Baltimore, Md. : 1950) 2005	SSLENFRAYV	Influenza A virus (A/Puerto Rico/8/34(H1N1)) Polymerase acidic protein (PA)	T + Cytokine Release-IFN-g
☐	Details	S M Mansour Haeryfar Journal of immunology (Baltimore, Md. : 1950) 2005	ASNENMETM	Influenza A virus (A/Puerto Rico/8/34(H1N1)) Nucleoprotein	T + Cytokine Release-IFN-g
☐	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	LYQNVGTYV	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☐	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	IYATVAGSL	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☐	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	TYVSVGTST	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☐	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	TYQRTRALV	Influenza A virus (A/Japan/305/57(H2N2)) Nucleoprotein	T + Cytokine Release-IFN-g

9 items found, displaying all items.
Page **1**

Export all results: Excel

Help us make the IEDB better by reporting erroneous entries

Much of the information contained in the IEDB is manually extracted by experts from scientific literature using significant effort to ensure accuracy. If you recognize an error or misinterpretation, we would greatly appreciate your help by using the feedback form to report any potential problems you observe. Please be sure to include (1) the IEDB identifier of the problematic record, (2) the field name(s) in which the problem is located, and (3) the corrected field values

Display Settings:

Format: Summary

Show: 10

Options:

[New Query]
[Revise Query]
[Save Query]
[View Query Details]
[Define Custom Report]

Analyze Selected Records:

Tool: T Cell Epitope Prediction

Analyze

9 items found, displaying all items.
Page **1**

	Links	Reference	Structure	Source	Assay
☑	Details	Samita S Andreansky Journal of virology. 2005	RTFSFQLI	Influenza A virus (A/PR/8/34(H1N1)) NS2	T + Cytokine Release-IFN-g
☐	Details	Samita S Andreansky Journal of virology. 2005	LSLRNPILV	Influenza A virus (A/PR/8/34(H1N1)) PB1-F2	T + Cytokine Release-IFN-g
☑	Details	David H Canaday Journal of immunological methods. 2003	GLKGGPSTE	Influenza A virus (A/PR/8/34(H1N1)) Matrix protein 2	T + Cytokine Release-IFN-g
☑	Details	S M Mansour Haeryfar Journal of immunology (Baltimore, Md. : 1950) 2005	SSLENFRAYV	Influenza A virus (A/Puerto Rico/8/34(H1N1)) Polymerase acidic protein (PA)	T + Cytokine Release-IFN-g
☑	Details	S M Mansour Haeryfar Journal of immunology (Baltimore, Md. : 1950) 2005	ASNENMETM	Influenza A virus (A/Puerto Rico/8/34(H1N1)) Nucleoprotein	T + Cytokine Release-IFN-g
☑	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	LYQNVGTYV	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☐	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	IYATVAGSL	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☐	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	TYVSVGTST	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☑	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	TYQRTRALV	Influenza A virus (A/Japan/305/57(H2N2)) Nucleoprotein	T + Cytokine Release-IFN-g

9 items found, displaying all items.
Page **1**

Export all results: Excel

Help us make the IEDB better by reporting erroneous entries

Much of the information contained in the IEDB is manually extracted by experts from scientific literature using significant effort to ensure accuracy. If you recognize an error or misinterpretation, we would greatly appreciate your help by using the feedback form to report any potential problems you observe. Please be sure to include (1) the IEDB identifier of the problematic record, (2) the field name(s) in which the problem is located, and (3) the corrected field values

Immune Epitope Database and Analysis Resource - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

Display Settings:

Format: Summary

Show: 10

Options:

[New Query]
[Revise Query]
[Save Query]
[View Query Details]
[Define Custom Report]

Analyze Selected Records:

Tool: T Cell Epitope Prediction

- T Cell Epitope Prediction
- B Cell Epitope Prediction
- Conservancy Analysis
- Population Coverage
- Homology Mapping

9 items found, displaying all items.
Page **1**

	Links	Reference	Structure	Source	Assay
☑	Details	Samita S Andreansky Journal of virology. 2005	RTFSFQLI	Influenza A virus (A/PR/8/34(H1N1)) NS2	T + Cytokine Release-IFN-g
☐	Details	Samita S Andreansky Journal of virology. 2005	LSLRNPILV	Influenza A virus (A/PR/8/34(H1N1)) PB1-F2	T + Cytokine Release-IFN-g
☑	Details	David H Canaday Journal of immunological methods. 2003	GLKGGPSTE	Influenza A virus (A/PR/8/34(H1N1)) Matrix protein 2	T + Cytokine Release-IFN-g
☑	Details	S M Mansour Haeryfar Journal of immunology (Baltimore, Md. : 1950) 2005	SSLENFRAYV	Influenza A virus (A/Puerto Rico/8/34(H1N1)) Polymerase acidic protein (PA)	T + Cytokine Release-IFN-g
☑	Details	S M Mansour Haeryfar Journal of immunology (Baltimore, Md. : 1950) 2005	ASNENMETM	Influenza A virus (A/Puerto Rico/8/34(H1N1)) Nucleoprotein	T + Cytokine Release-IFN-g
☑	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	LYQNVGTYV	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☐	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	IYATVAGSL	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☐	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	TYVSVGTST	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☑	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	TYQRTRALV	Influenza A virus (A/Japan/305/57(H2N2)) Nucleoprotein	T + Cytokine Release-IFN-g

9 items found, displaying all items.
Page **1**

Export all results: Excel

Help us make the IEDB better by reporting erroneous entries

Much of the information contained in the IEDB is manually extracted by experts from scientific literature using significant effort to ensure accuracy. If you recognize an error or misinterpretation, we would greatly appreciate your help by using the feedback form to report any potential problems you observe. Please be sure to include (1) the IEDB identifier of the problematic record, (2) the field name(s) in which the problem is located, and (3) the corrected field values

Immune Epitope Database and Analysis Resource - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

Display Settings:

Format: Summary

Show: 10

Options:

[New Query]
[Revise Query]
[Save Query]
[View Query Details]
[Define Custom Report]

Analyze Selected Records:

Tool: T Cell Epitope Prediction

Analyze

9 items found, displaying all items.
Page **1**

	Links	Reference	Structure	Source	Assay
☑	Details	Samita S Andreansky Journal of virology. 2005	RTFSFQLI	Influenza A virus (A/PR/8/34(H1N1)) NS2	T + Cytokine Release-IFN-g
☐	Details	Samita S Andreansky Journal of virology. 2005	LSLRNPILV	Influenza A virus (A/PR/8/34(H1N1)) PB1-F2	T + Cytokine Release-IFN-g
☑	Details	David H Canaday Journal of immunological methods. 2003	GLKGGPSTE	Influenza A virus (A/PR/8/34(H1N1)) Matrix protein 2	T + Cytokine Release-IFN-g
☑	Details	S M Mansour Haeryfar Journal of immunology (Baltimore, Md. : 1950) 2005	SSLENFRAYV	Influenza A virus (A/Puerto Rico/8/34(H1N1)) Polymerase acidic protein (PA)	T + Cytokine Release-IFN-g
☑	Details	S M Mansour Haeryfar Journal of immunology (Baltimore, Md. : 1950) 2005	ASNENMETM	Influenza A virus (A/Puerto Rico/8/34(H1N1)) Nucleoprotein	T + Cytokine Release-IFN-g
☑	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	LYQNVGTYV	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☐	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	IYATVAGSL	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☐	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	TYVSVGTST	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☑	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	TYQRTRALV	Influenza A virus (A/Japan/305/57(H2N2)) Nucleoprotein	T + Cytokine Release-IFN-g

9 items found, displaying all items.
Page **1**

Export all results: Excel

Help us make the IEDB better by reporting erroneous entries

Much of the information contained in the IEDB is manually extracted by experts from scientific literature using significant effort to ensure accuracy. If you recognize an error or misinterpretation, we would greatly appreciate your help by using the feedback form to report any potential problems you observe. Please be sure to include (1) the IEDB identifier of the problematic record, (2) the field name(s) in which the problem is located, and (3) the corrected field values

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

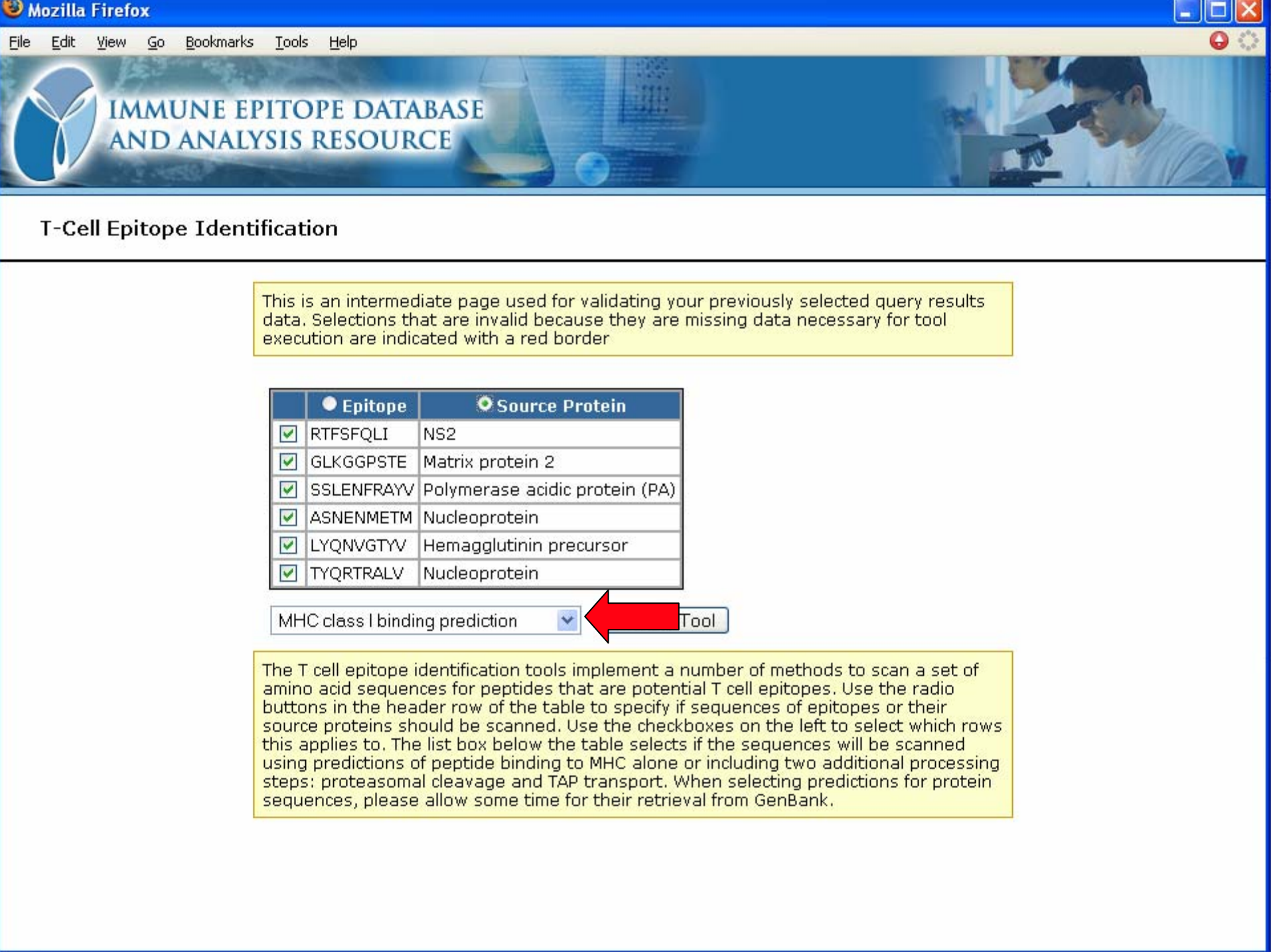
T-Cell Epitope Identification

This is an intermediate page used for validating your previously selected query results data. Selections that are invalid because they are missing data necessary for tool execution are indicated with a red border

	Epitope	Source Protein
☑	RTFSFQLI	NS2
☑	GLKGGPSTE	Matrix protein 2
☑	SSLENFRAYV	Polymerase acidic protein (PA)
☑	ASNENMETM	Nucleoprotein
☑	LYQNVGTYV	Hemagglutinin precursor
☑	TYQRTRALV	Nucleoprotein

MHC class I binding prediction | Send to Tool

The T cell epitope identification tools implement a number of methods to scan a set of amino acid sequences for peptides that are potential T cell epitopes. Use the radio buttons in the header row of the table to specify if sequences of epitopes or their source proteins should be scanned. Use the checkboxes on the left to select which rows this applies to. The list box below the table selects if the sequences will be scanned using predictions of peptide binding to MHC alone or including two additional processing steps: proteasomal cleavage and TAP transport. When selecting predictions for protein sequences, please allow some time for their retrieval from GenBank.


Mozilla Firefox
File Edit View Go Bookmarks Tools Help
IMMUNE EPITOPE DATABASE
AND ANALYSIS RESOURCE
T-Cell Epitope Identification
This is an intermediate page used for validating your previously selected query results data. Selections that are invalid because they are missing data necessary for tool execution are indicated with a red border
Epitope
Source Protein
RTFSFQLI NS2
GLKGGPSTE Matrix protein 2
SSLENFRAYV Polymerase acidic protein (PA)
ASNENMETM Nucleoprotein
LYQNVGTYV Hemagglutinin precursor
TYQRTRALV Nucleoprotein
MHC class I binding prediction
Tool
The T cell epitope identification tools implement a number of methods to scan a set of amino acid sequences for peptides that are potential T cell epitopes. Use the radio buttons in the header row of the table to specify if sequences of epitopes or their source proteins should be scanned. Use the checkboxes on the left to select which rows this applies to. The list box below the table selects if the sequences will be scanned using predictions of peptide binding to MHC alone or including two additional processing steps: proteasomal cleavage and TAP transport. When selecting predictions for protein sequences, please allow some time for their retrieval from GenBank.

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

T-Cell Epitope Identification

This is an intermediate page used for validating your previously selected query results data. Selections that are invalid because they are missing data necessary for tool execution are indicated with a red border

	Epitope	Source Protein
☑	RTFSFQLI	NS2
☑	GLKGGPSTE	Matrix protein 2
☑	SSLENFRAYV	Polymerase acidic protein (PA)
☑	ASNENMETM	Nucleoprotein
☑	LYQNVGTYV	Hemagglutinin precursor
☑	TYQRTRALV	Nucleoprotein

MHC class I binding prediction | Send to Tool

MHC class I binding prediction
MHC class I processing prediction
MHC class II binding prediction

T[illegible]mplement a number of methods to scan a set of a[illegible]t are potential T cell epitopes. Use the radio buttons in the header row of the table to specify if sequences of epitopes or their source proteins should be scanned. Use the checkboxes on the left to select which rows this applies to. The list box below the table selects if the sequences will be scanned using predictions of peptide binding to MHC alone or including two additional processing steps: proteasomal cleavage and TAP transport. When selecting predictions for protein sequences, please allow some time for their retrieval from GenBank.

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

MHC-I binding predictions

- Prediction Home
- Tutorial
- Example Data

Specify Sequence(s)

Enter protein sequence(s):

```
>138967|Nonstructural protein NS2
MDPNTVSSFQDILLRMSKMQLESSSGDLNGMITQFESLKLYRDSLGEAVMRMGDLHSLQN
RNEKWREQLGQKFEEIRWLIEEVRHKLKITENSFEQITFMQALHLLLEVEQEIRTFSFQL
I
>56583270|matrix protein 2 [Influenza A virus]
MSLLTEVETPIRNEWGCRCNGSSDPLAIAANIIGILHLILWILDRLFFKCIYRRFKYGLK
GGPSTEGVPKSMREEYRKEQQSAVDADDGHFVSIELE
>133544|RNA-directed RNA polymerase subunit P2 (Polymerase
acidic protein) (PA)
```

Or select file containing sequence(s): Browse...

Choose sequence format: auto detect format

Specify what to make binding predictions for

MHC source species: mouse

MHC allele: H-2 Db

Peptide length: 9

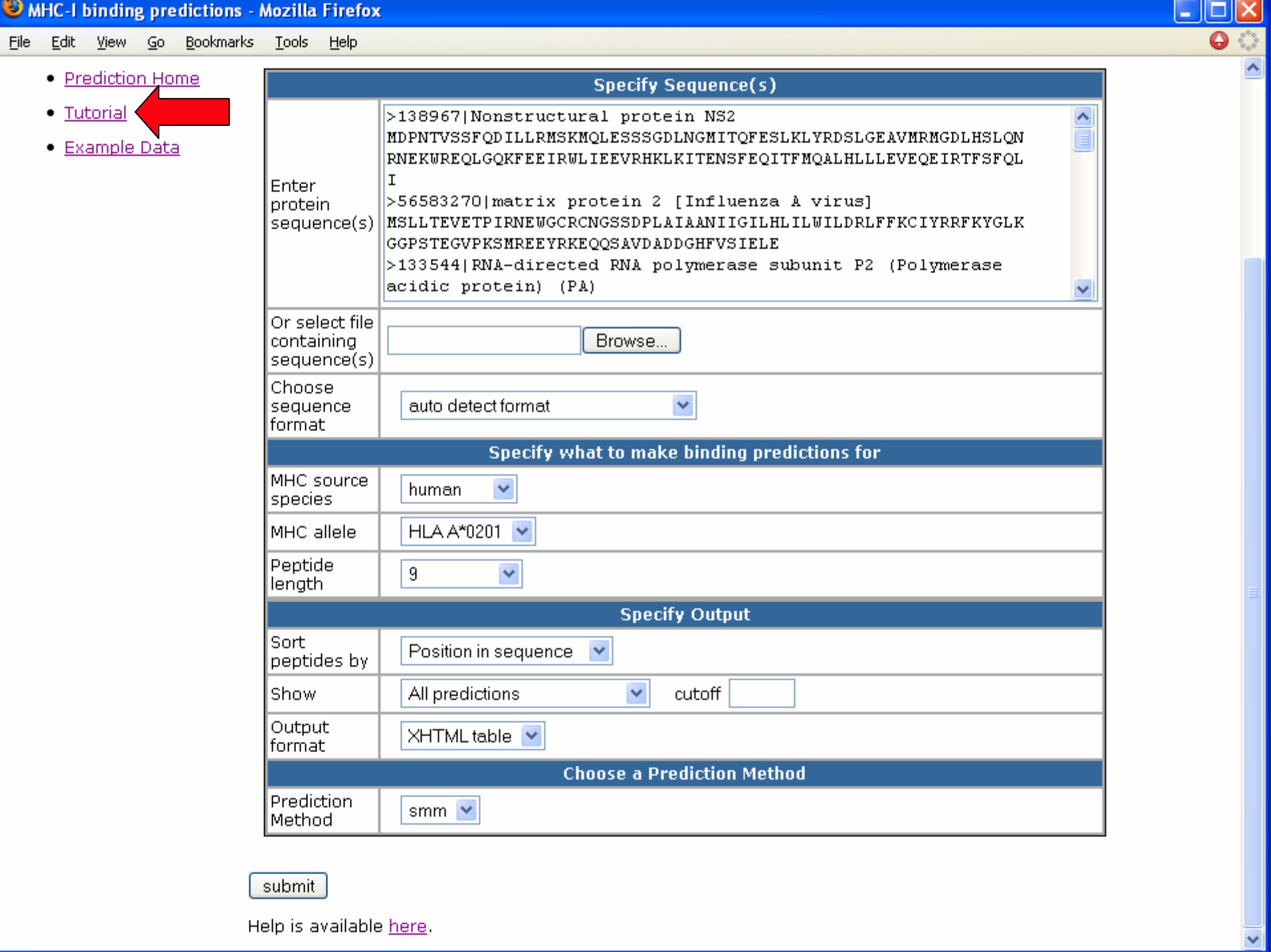
Specify Output

Sort peptides by: Position in sequence

Show: All predictions cutoff

Outline

- Tool integration
- T cell epitope identification tools
- B cell epitope identification tools
- Epitope analysis tools
- Visualization tools


MHC-I binding predictions - Mozilla Firefox
File Edit View Go Bookmarks Tools Help
Prediction Home
Tutorial
Example Data
Specify Sequence(s)
Enter protein sequence(s)
>138967|Nonstructural protein NS2
MDPNTVSSFQDILLRMSKMQLESSSGDLNGMITQFESLKLYRDSLGEAVMRMGDLHSLQN
RNEKWREQLGQKFEEIRWLIEEVRHKLKITENSFEQITFMQALHLLLEVEQEIRTFSFQL
I
>56583270|matrix protein 2 [Influenza A virus]
MSLLTEVETPIRNEWGCRCNGSSDPLAIAANIIGILHLILWILDRLFFKCIYRRFKYGLK
GGPSTEGVPKSMREEYRKEQQSAVDADDGHFVSIELE
>133544|RNA-directed RNA polymerase subunit P2 (Polymerase
acidic protein) (PA)
Or select file containing sequence(s)
Browse...
Choose sequence format
auto detect format
Specify what to make binding predictions for
MHC source species
human
MHC allele
HLA A*0201
Peptide length
9
Specify Output
Sort peptides by
Position in sequence
Show
All predictions
cutoff
Output format
XHTML table
Choose a Prediction Method
Prediction Method
smm
submit
Help is available here.

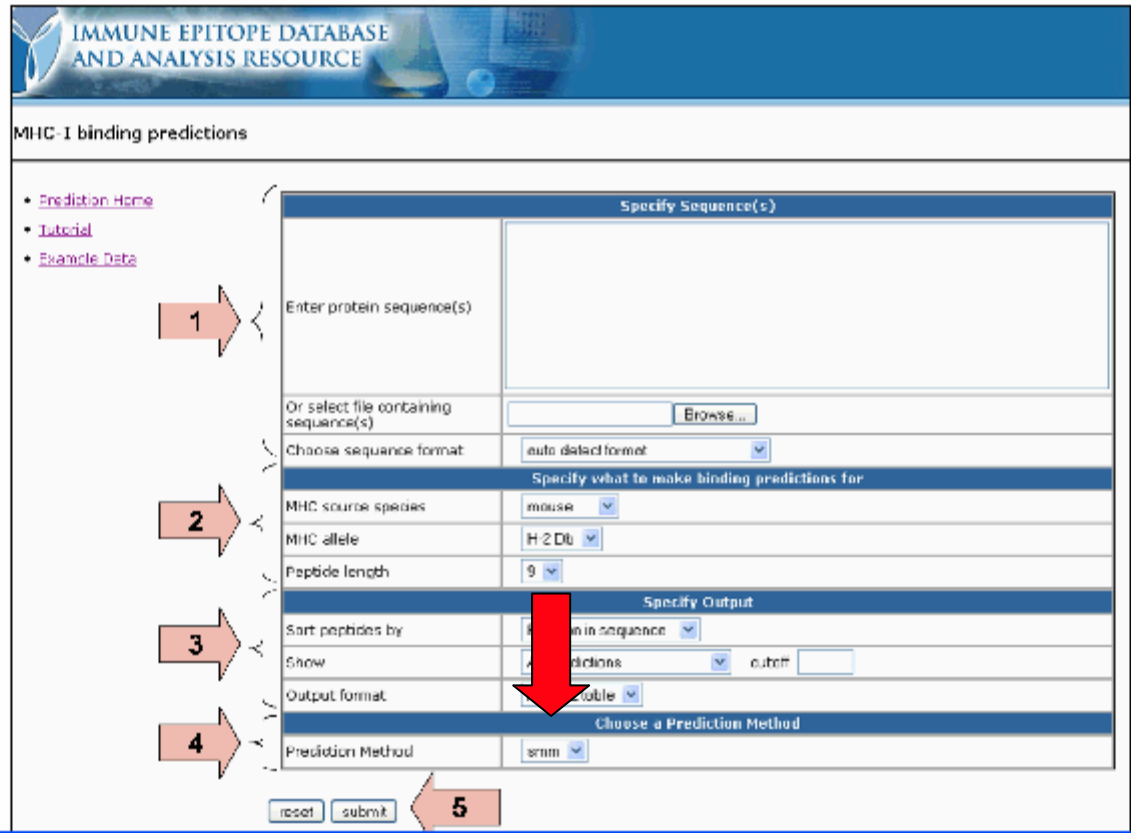
IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

MHC-I binding predictions - Tutorial

- Prediction Home
- Tutorial
- Example Data

How to obtain predictions

This website provides access to predictions of peptide binding to MHC class I molecules. The screenshot below illustrates the steps necessary to make a prediction. Each of the steps is described in more detail below.



1. Specify sequences

First specify the sequences you want to scan for binding peptides. The sequences should either be entered directly into the textarea field labeled "Enter protein sequence(s), or can be taken from a file that has to be uploaded using the button labeled "Browse".

The sequences can be supplied in three different formats:

- Space separated sequences
- One continuous sequence
- FASTA format

The format of the sequences can be specified explicitly using the list box labeled "Choose sequence format". If that list box is set to "auto detect format", the input will be interpreted as FASTA if an opening ">" character is found, or as a continuous sequence otherwise.

All sequences have to be amino acids specified in single letter code (`ACDEFGHIKLMNPQRSTVWY`)

2. Specify what to make predictions for

Predictions are limited to peptides of one specific length binding to one specific allele at a time. The allele / peptide length combination can be selected using the list boxes in this section. For some allele / peptide length combinations, no prediction tools exist because there is too little experimental data available to generate them.

Selections in the listboxes in this section influence the values available in others. For example, selecting "mouse" as the MHC source species will limit the selections available in the MHC allele listbox. Similarly, the allele chosen will limit the available peptide lengths.

3. Specify the output

The menus in this section change how th rediction output is displayed. Using the "Sort peptides by" listbox, the results can be p orted by the order of the peptides in their source sequence (default) or by their pr d affinity.

To limit the number of results displayed, which can significantly speed up the time it takes to make a prediction, it is possible to define an upper boundary for the prediction in the "cutoff" field. Note that the listbox preceding the "cutoff" field has to be set to "MHC predictions better than" for the cutoff to take effect.

To reuse the prediction results in an external program, it is possible to retrieve the predictions in a plain text format. To do this, choose "Text file" in the output format listbox.

4. Choose a prediction method

The prediction method list box allows choosing between three currently implemented MHC class I binding prediction methods:

- Artificial neural network (ann)
- Average relative binding (arb)
- Stabilized matrix method (smm)

Please note that changing the prediction method can influence what allele / peptide length combinations are available in section 2. For example, the neural network prediction is currently limited to peptides of length 9.

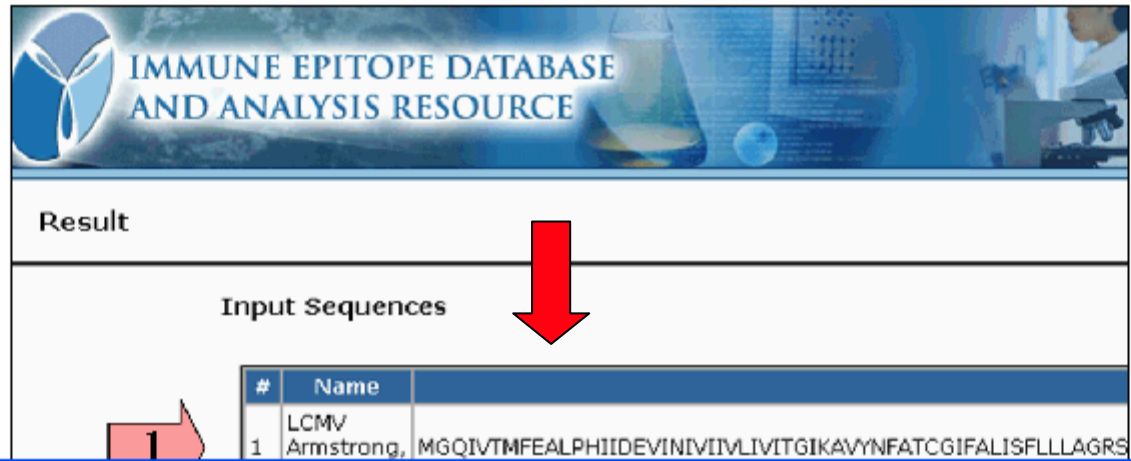
The IEDB team is in the process of making a formalized comparison of the performance of the three methods. Until that is completed, no guidance can be given as to which method should be chosen.

5. Submit the prediction

This one is easy. Click the submit button, and a result screen similar to the one below should appear.

Interpreting prediction output

Below is a screenshot of a prediction output page, with four relevant sections marked that are described in more detail below.



H-2 Db	1:3-11	9	QIVTMFEAL	681.1
H-2 Db	1:4-12	9	IVTMFEALP	4122.1
H-2 Db	1:5-13	9	VTMFEALPH	3507.9
H-2 Db	1:6-14	9	TMFEALPHI	191.7
H-2 Db	1:7-15	9	MFEALPHII	7400.6
H-2 Db	1:8-16	9	FEALPHIID	46816.8
H-2 Db	1:9-17	9	EALPHIIDE	308.0
H-2 Db	1:10-18	9	ALPHIIDEV	1715.5
H-2 Db	1:11-19	9	LPHIIDEVI	9276.8

1. Input Sequences

This table displays the sequences and their names extracted from the user input. If no names were assigned by the user (which is only possible in FASTA format), the sequences are numbered in their input order (sequence 1, sequence 2, ...).

2. Filter predictions

By adding a cutoff in the input field and clicking the "Add Filter" button, only peptides with an affinity better than the cutoff value are displayed.

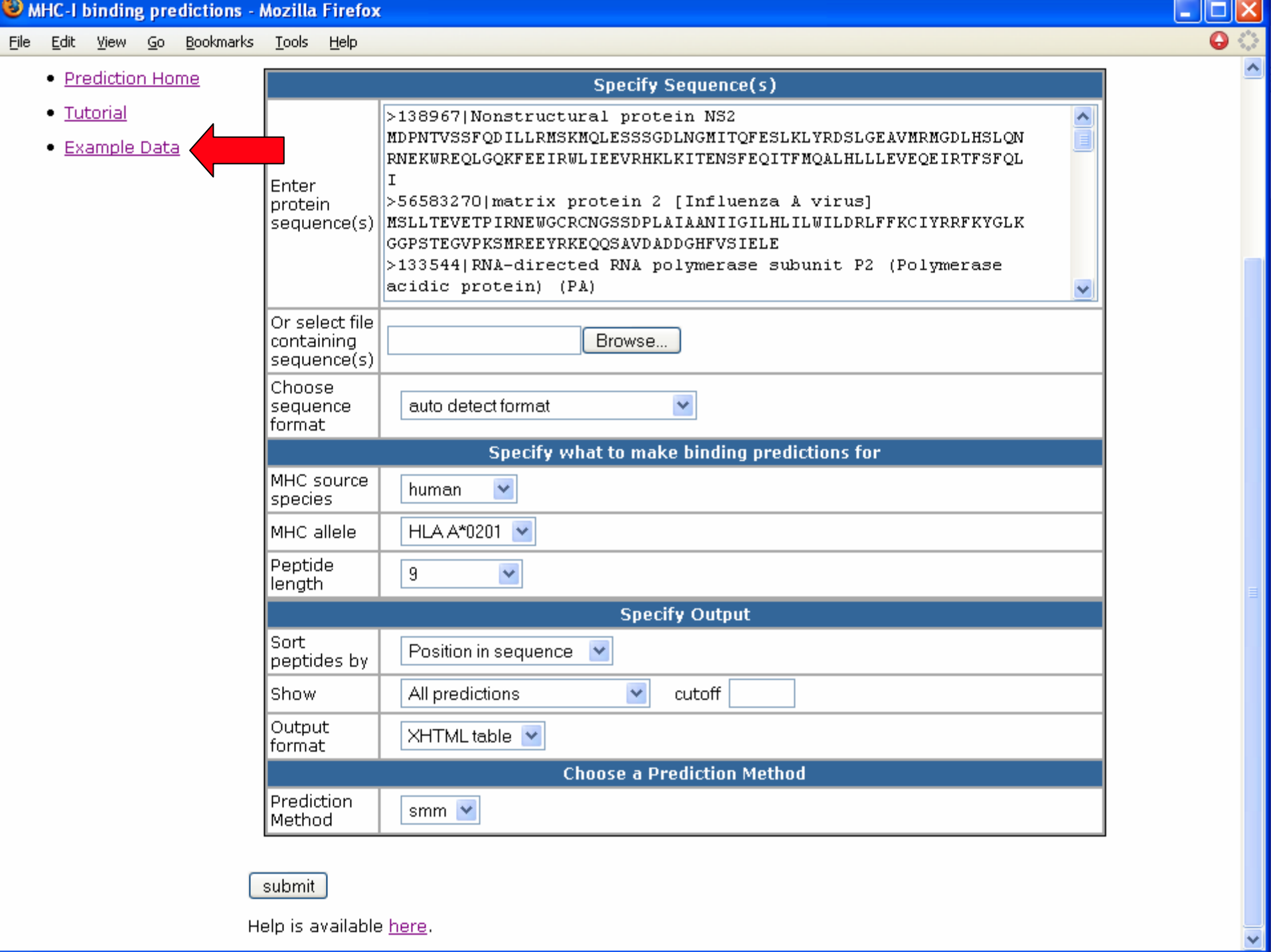
3. Prediction output table

Each row in this table corresponds to one peptide binding prediction. The columns contain the allele the prediction was made for, the position of the peptide in the input sequences (in the format [Sequence #]: [Start Position] - [End Position]), the length of the peptide, the peptide sequence and the predicted affinity. The table can be sorted by clicking on the table column headers.

4. Interpreting predicted affinities

The predicted output is given in units of IC_{50}nM. Therefore a lower number indicates higher affinity. As a rough guideline, peptides with IC_{50} values <50 nM are considered high affinity, <500 nM intermediate affinity and <5000 nM low affinity. Most known epitopes have high or intermediate affinity. Some epitopes have low affinity, but no known T-cell epitope has an IC_{50} value greater than 5000.

While the output of the predictions is quantitative, there are systematic deviations from experimental IC_{50} values. For example, the makeup of the training data and the prediction methods used have a non-trivial impact on the range of predicted IC_{50} values. A detailed evaluation of the correlation between predicted IC50 and antigenicity of peptides is currently being conducted which will help to better interpret prediction results.


MHC-I binding predictions - Mozilla Firefox
File Edit View Go Bookmarks Tools Help
Prediction Home
Tutorial
Example Data
Specify Sequence(s)
Enter protein sequence(s)
>138967|Nonstructural protein NS2
MDPNTVSSFQDILLRMSKMQLESSSGDLNGMITQFESLKLYRDSLGEAVMRMGDLHSLQN
RNEKWREQLGQKFEEIRWLIEEVRHKLKITENSFEQITFMQALHLLLEVEQEIRTFSFQL
I
>56583270|matrix protein 2 [Influenza A virus]
MSLLTEVETPIRNEWGCRCNGSSDPLAIAANIIGILHLILWILDRLFFKCIYRRFKYGLK
GGPSTEGVPKSMREEYRKEQQSAVDADDGHFVSIELE
>133544|RNA-directed RNA polymerase subunit P2 (Polymerase
acidic protein) (PA)
Or select file containing sequence(s)
Browse...
Choose sequence format
auto detect format
Specify what to make binding predictions for
MHC source species
human
MHC allele
HLA A*0201
Peptide length
9
Specify Output
Sort peptides by
Position in sequence
Show
All predictions
cutoff
Output format
XHTML table
Choose a Prediction Method
Prediction Method
smm
submit
Help is available here.

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

MHC-I binding predictions - Example data

- Prediction Home
- Tutorial
- Example Data

Choose one of the radio buttons below to select protein sequence(s) containing MHC class I epitopes described in the literature with defined MHC restrictions for which predictions are available. These sequences will be transfered to the MHC class I binding predictions when clicking the "Submit" button. These test-datasets are meant to demonstrate the functionality of the tools and are by no means considered equivalent to a formal performance evaluation.

(•) GP and NP protein of LCMV virus strain armstrong

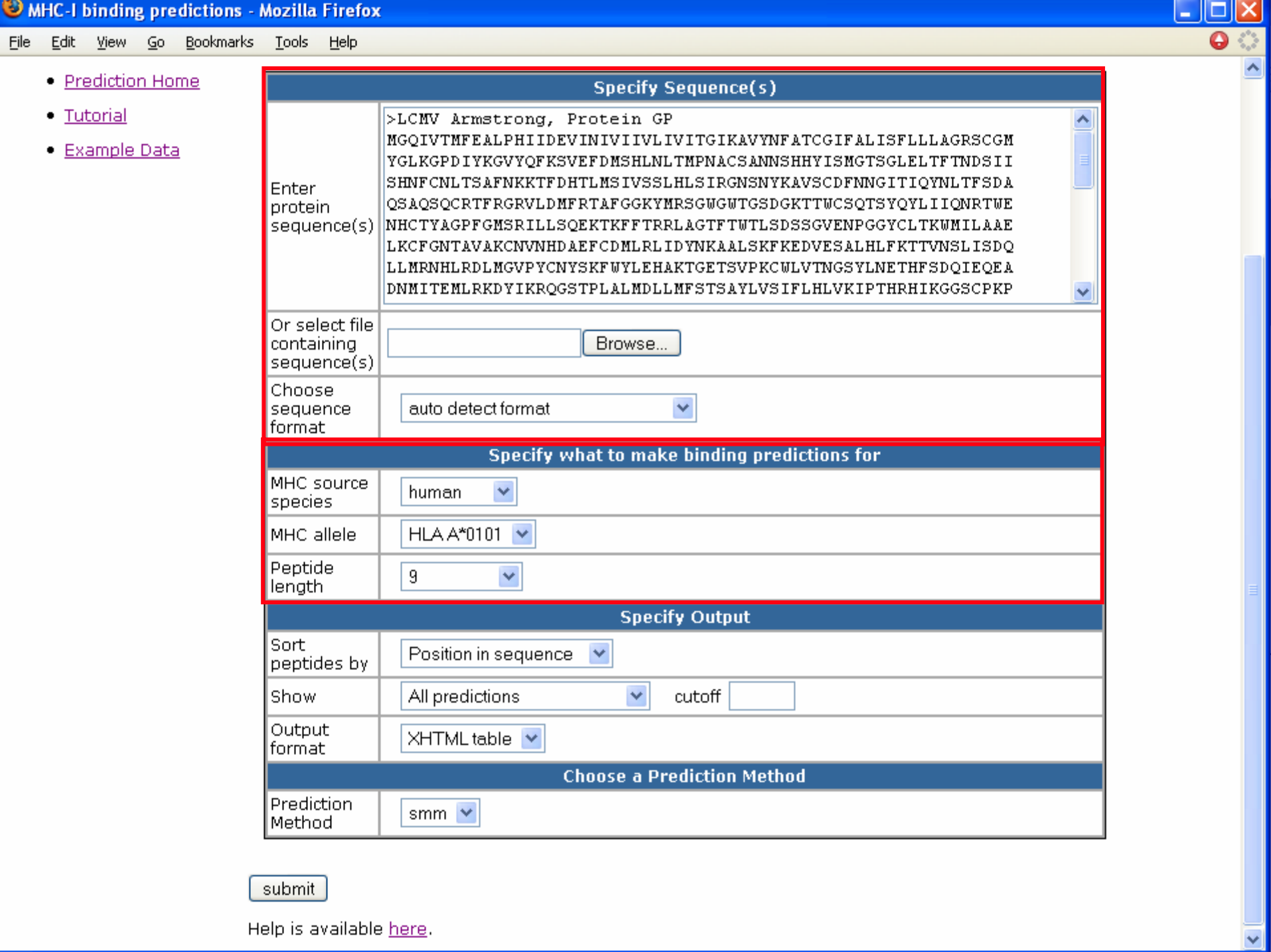
Peptide	Length	MHC restriction
FQPQNGQFI	9	H-2 Db
KAVYNFATC	9	H-2 Db
ISHNFCNL	8	H-2 Kb
YTVKYPNL	8	H-2 Kb

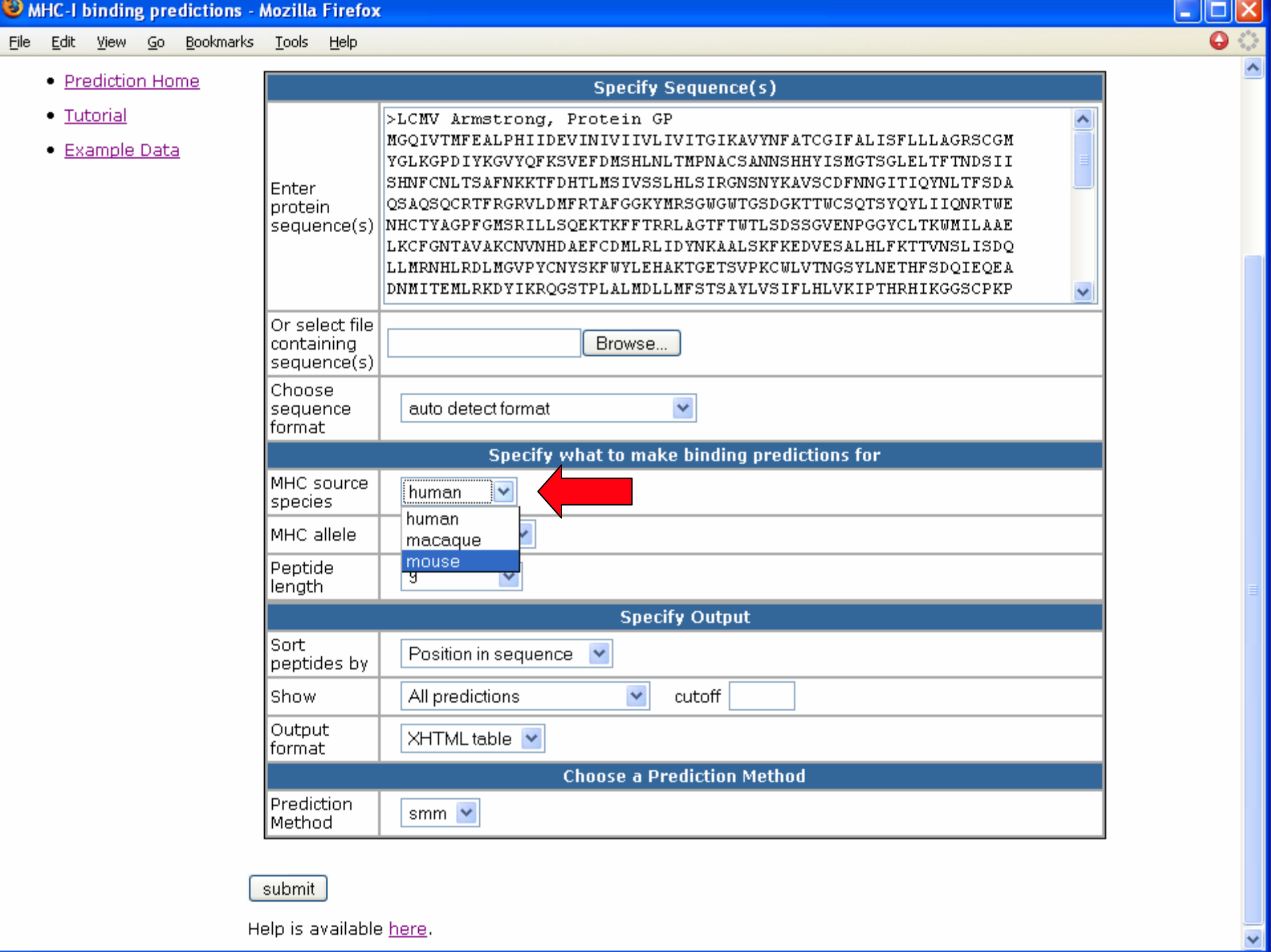
( ) SARS spike protein

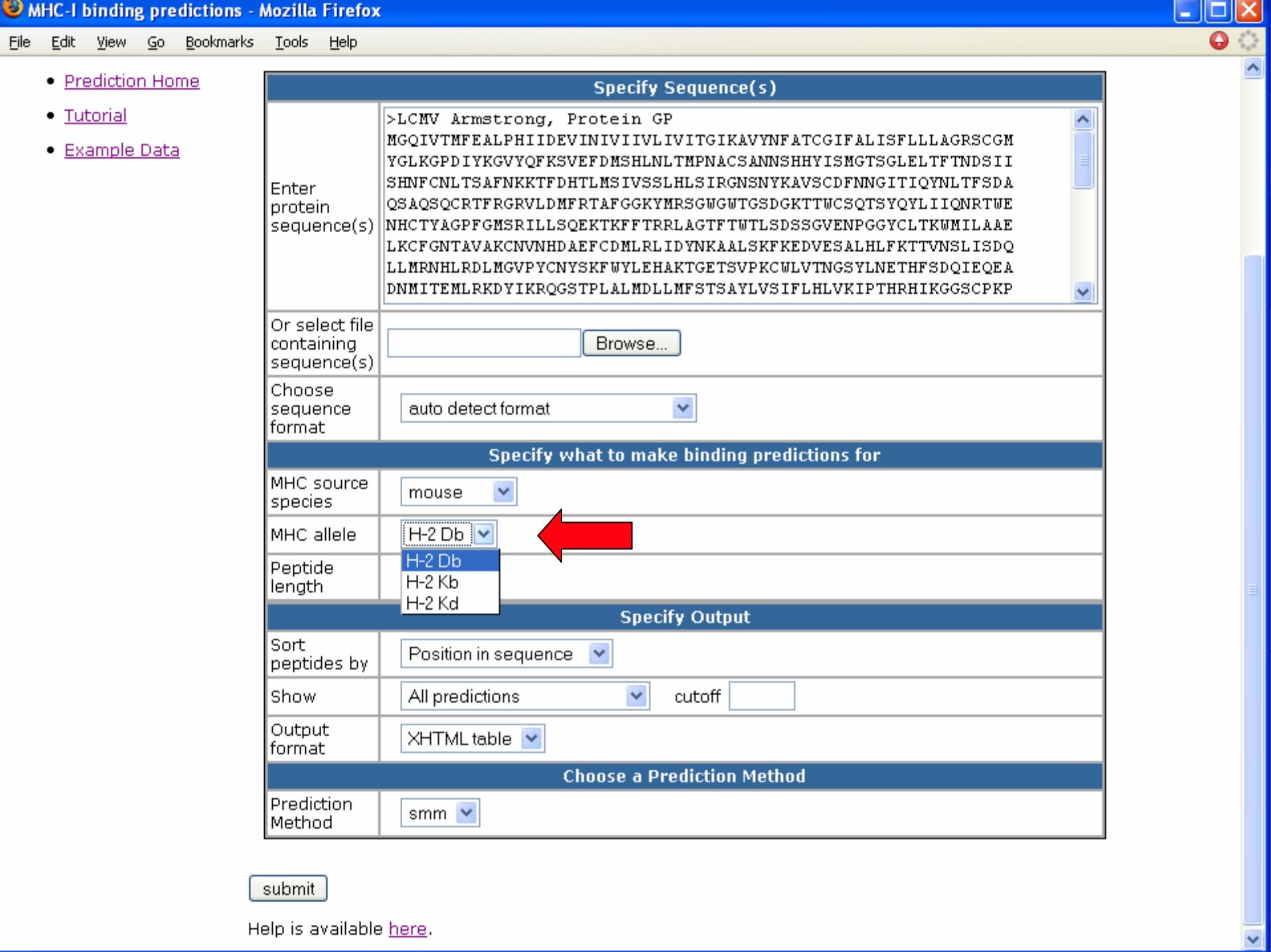
Peptide	Length	MHC restriction
FIAGLIAIV	9	HLA A*0201
LITGRLQSL	9	HLA A*0201
RLNEVAKNL	9	HLA A*0201

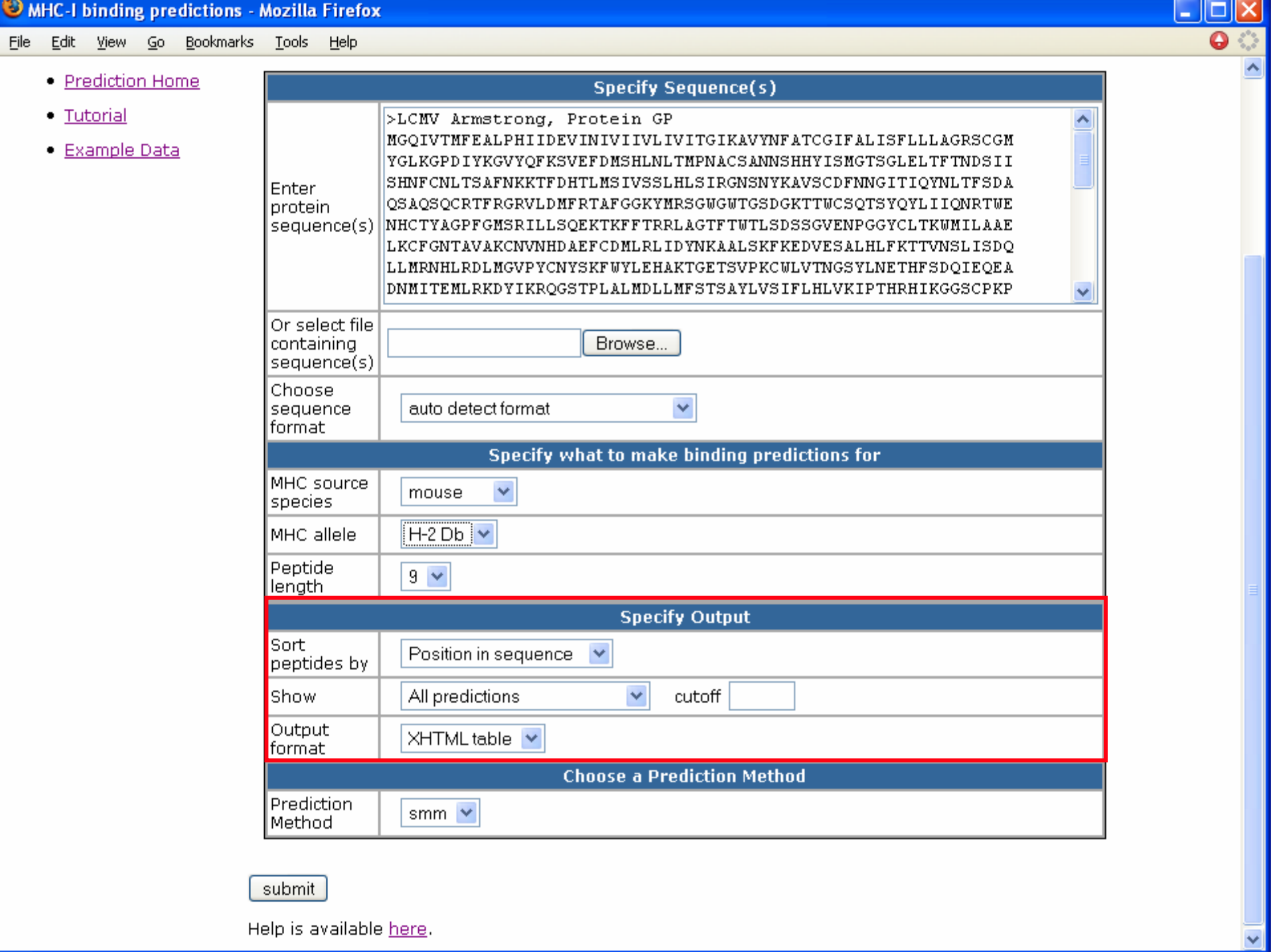
Submit

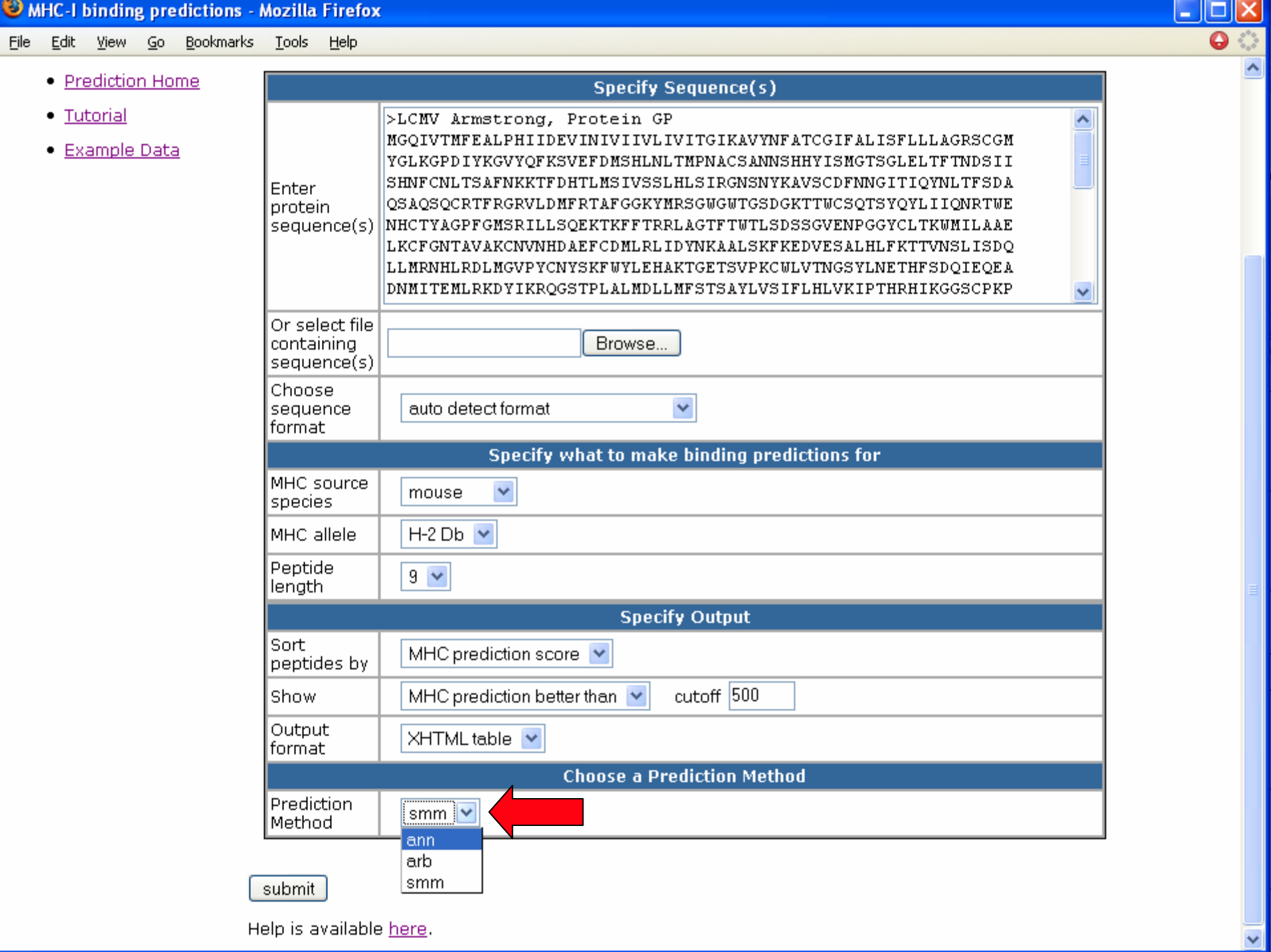
You can also use these sequences with MHC class I processing predictions

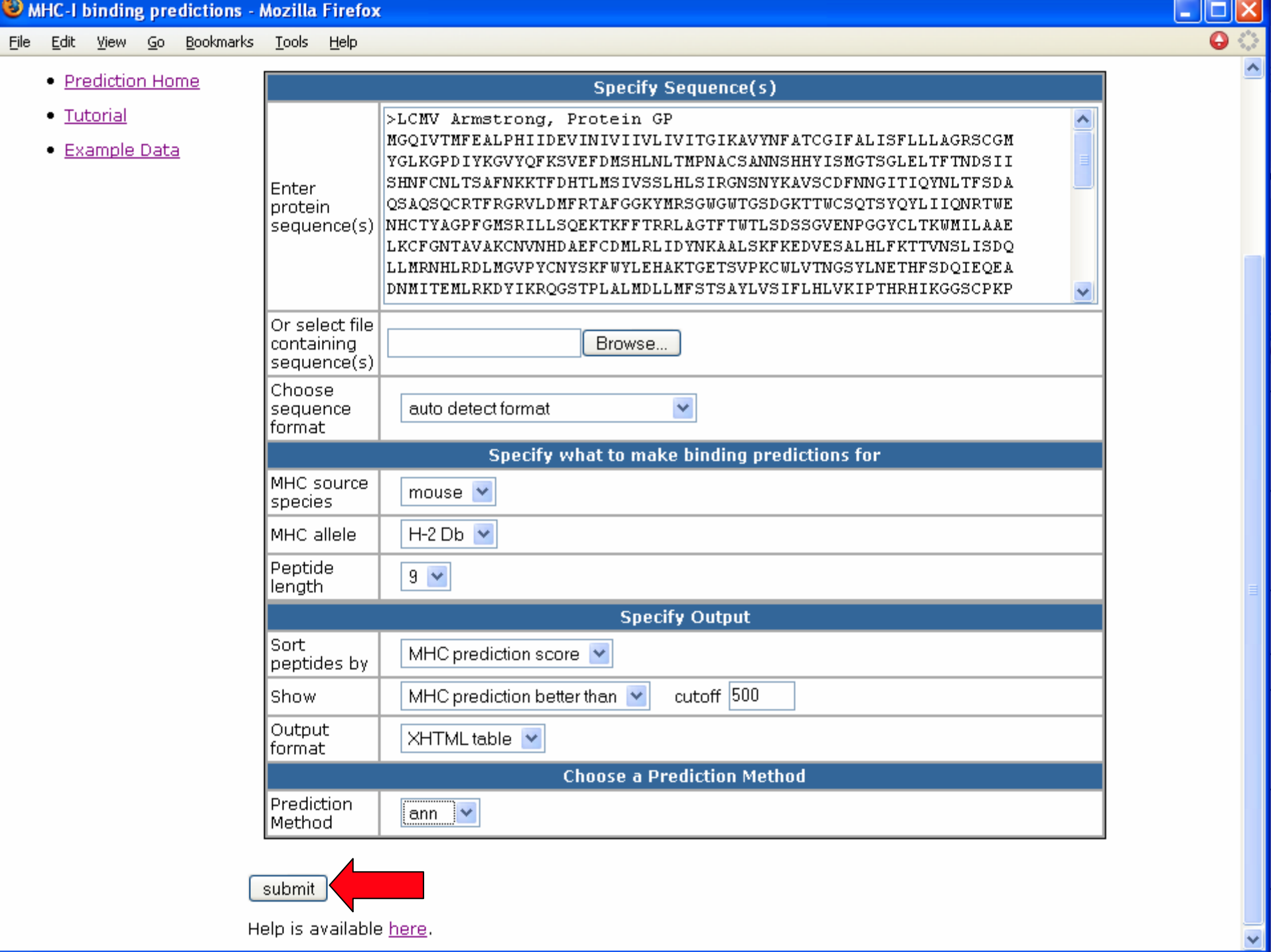

MHC-I binding predictions - Mozilla Firefox
File Edit View Go Bookmarks Tools Help
Prediction Home
Tutorial
Example Data
Specify Sequence(s)
Enter protein sequence(s)
>LCMV Armstrong, Protein GP
MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM
YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII
SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA
QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE
NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE
LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ
LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA
DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP
Or select file containing sequence(s)
Browse...
Choose sequence format
auto detect format
Specify what to make binding predictions for
MHC source species
human
MHC allele
HLA A*0101
Peptide length
9
Specify Output
Sort peptides by
Position in sequence
Show
All predictions
cutoff
Output format
XHTML table
Choose a Prediction Method
Prediction Method
smm
submit
Help is available here.


MHC-I binding predictions - Mozilla Firefox
File Edit View Go Bookmarks Tools Help
Prediction Home
Tutorial
Example Data
Specify Sequence(s)
Enter protein sequence(s)
>LCMV Armstrong, Protein GP
MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM
YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII
SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA
QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE
NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE
LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ
LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA
DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP
Or select file containing sequence(s)
Browse...
Choose sequence format
auto detect format
Specify what to make binding predictions for
MHC source species
human
human
macaque
mouse
MHC allele
Peptide length
Specify Output
Sort peptides by
Position in sequence
Show
All predictions
cutoff
Output format
XHTML table
Choose a Prediction Method
Prediction Method
smm
submit
Help is available here.


MHC-I binding predictions - Mozilla Firefox
File Edit View Go Bookmarks Tools Help
Prediction Home
Tutorial
Example Data
Specify Sequence(s)
Enter protein sequence(s)
>LCMV Armstrong, Protein GP
MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM
YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII
SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA
QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE
NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE
LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ
LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA
DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP
Or select file containing sequence(s)
Browse...
Choose sequence format
auto detect format
Specify what to make binding predictions for
MHC source species
mouse
MHC allele
H-2 Db
H-2 Db
H-2 Kb
H-2 Kd
Peptide length
Specify Output
Sort peptides by
Position in sequence
Show
All predictions
cutoff
Output format
XHTML table
Choose a Prediction Method
Prediction Method
smm
submit
Help is available here.


MHC-I binding predictions - Mozilla Firefox
File Edit View Go Bookmarks Tools Help
Prediction Home
Tutorial
Example Data
Specify Sequence(s)
Enter protein sequence(s)
>LCMV Armstrong, Protein GP
MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM
YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII
SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA
QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE
NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE
LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ
LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA
DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP
Or select file containing sequence(s)
Browse...
Choose sequence format
auto detect format
Specify what to make binding predictions for
MHC source species
mouse
MHC allele
H-2 Db
Peptide length
9
Specify Output
Sort peptides by
Position in sequence
Show
All predictions
cutoff
Output format
XHTML table
Choose a Prediction Method
Prediction Method
smm
submit
Help is available here.


MHC-I binding predictions - Mozilla Firefox
File Edit View Go Bookmarks Tools Help
Prediction Home
Tutorial
Example Data
Specify Sequence(s)
Enter protein sequence(s)
>LCMV Armstrong, Protein GP
MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM
YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII
SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA
QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE
NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE
LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ
LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA
DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP
Or select file containing sequence(s)
Browse...
Choose sequence format
auto detect format
Specify what to make binding predictions for
MHC source species
mouse
MHC allele
H-2 Db
Peptide length
9
Specify Output
Sort peptides by
MHC prediction score
Show
MHC prediction better than
cutoff
500
Output format
XHTML table
Choose a Prediction Method
Prediction Method
smm
ann
arb
smm
submit
Help is available here.


MHC-I binding predictions - Mozilla Firefox
File Edit View Go Bookmarks Tools Help
Prediction Home
Tutorial
Example Data
Specify Sequence(s)
Enter protein sequence(s)
>LCMV Armstrong, Protein GP
MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM
YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII
SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA
QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE
NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE
LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ
LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA
DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP
Or select file containing sequence(s)
Browse...
Choose sequence format
auto detect format
Specify what to make binding predictions for
MHC source species
mouse
MHC allele
H-2 Db
Peptide length
9
Specify Output
Sort peptides by
MHC prediction score
Show
MHC prediction better than
cutoff
500
Output format
XHTML table
Choose a Prediction Method
Prediction Method
ann
submit
Help is available here.

Result

- Prediction Home
- Tutorial
- Example Data

Input Sequences

#	Name	
1	LCMV Armstrong, Protein GP	MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGMYGLKGPDIYKGVYQFKSVEFDMSH
2	LCMV Armstrong, Protein NP	MSLSKEVKSFQWTQALRRELQSFTSDVKAAVIKDATNLLNGLDFSEVSNVQRIMRKEKRDDKDLQRLRSLNQTVHSLV

Predictions - Low IC50 values = good binders

Help is available here

Predicted IC50 [nM] < [ ] Add Filter

Allele	Position	PepLength	Sequence	IC50 [nM]
H-2 Db	2:246-254	9	AAVKAGAAL	5.0
H-2 Db	2:396-404	9	FQPQNGQFI	13.0
H-2 Db	1:353-361	9	DQLLMRNHL	17.9
H-2 Db	2:252-260	9	AALLDGGNM	20.8
H-2 Db	2:29-37	9	AAVIKDATN	22.2
H-2 Db	2:339-347	9	PAVNSPRPA	26.3
H-2 Db	1:434-442	9	LALMDLLMF	36.8
H-2 Db	1:33-41	9	KAVYNFATC	39.0
H-2 Db	1:38-46	9	FATCGIFAL	43.0
H-2 Db	1:44-52	9	FALISFLLL	43.0
H-2 Db	1:93-101	9	SANNSHHYI	43.9
H-2 Db	2:376-384	9	NAPTWIDIE	45.2
H-2 Db	2:276-284	9	KAVLGAKRK	45.6

T cell epitope identification

- More tools:
  - MHC class I processing predictions (Proteasome / TAP / MHC)
  - MHC class II binding predictions
- Ongoing evaluation
  - transparent process
  - public datasets
- Machine interface

Outline

- Tool integration
- T cell epitope identification tools
- B cell epitope identification tools
- Epitope analysis tools
- Visualization tools

Scope

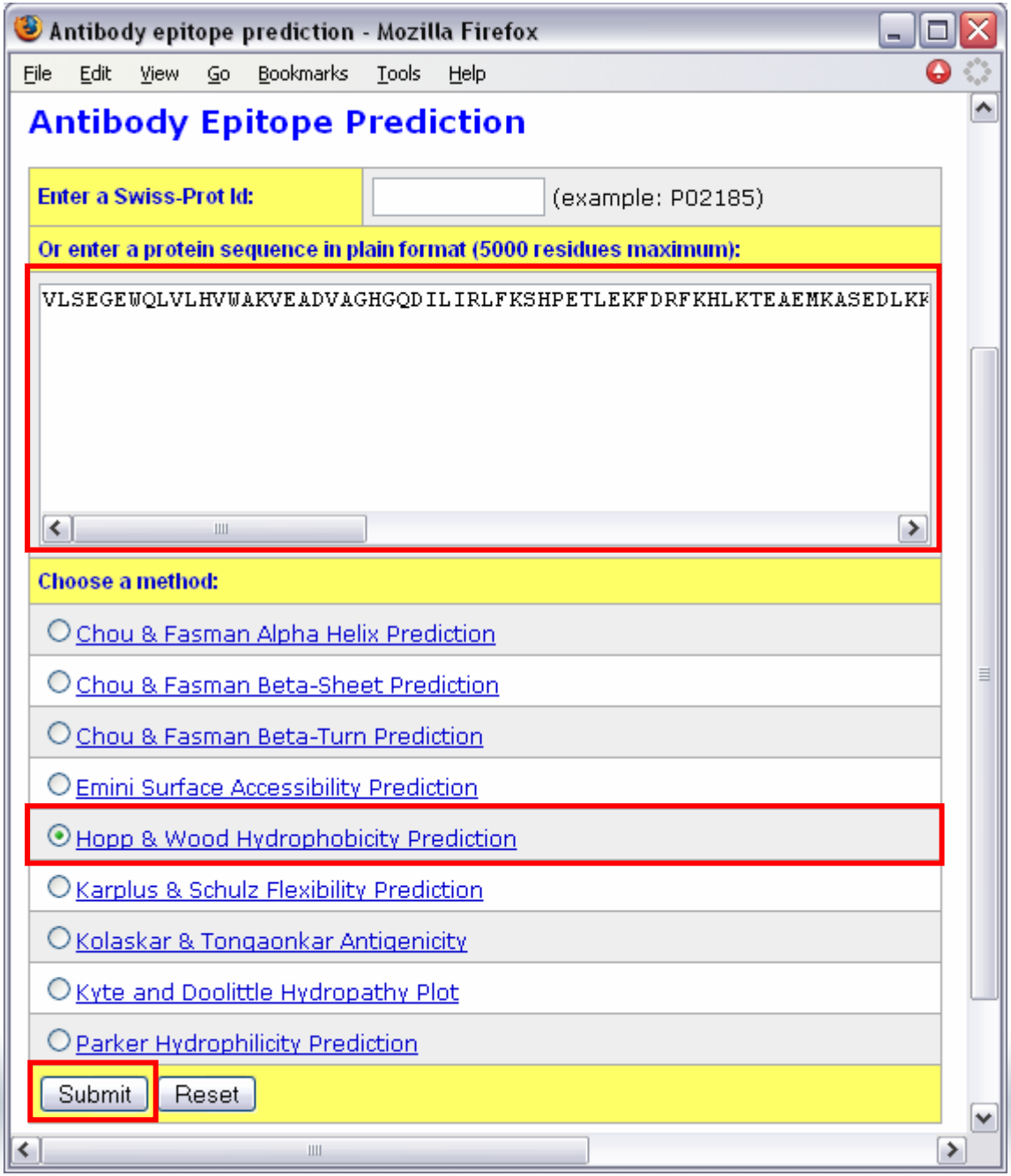
- Types of antibody epitope
  - Continuous
  - Discontinuous
- Aim of 1st release:
  - Implementation of methods for predicting continuous antibody epitope from protein sequences

General Basis

- Locations of continuous epitopes within protein sequences have been correlated with different parameters such as:
  - Hydrophilicity
  - Flexibility
  - Accessibility
  - Turns
  - Exposed surface
  - Polarity
  - Antigenic propensity
  - …
- This has led to a search for empirical rules that would allow the position of continuous epitopes to be predicted from certain features of the protein sequence.

Implemented Methods

- Hyrophobicity/hydrophilicity
  - Hopp and Wood hydrophobicity prediction
  - Parker hydrophilicity prediction
  - Kyte and Doolittle hydropathy plot
- Secondary structure
  - Chou & Fasman alpha helix prediction
  - Chou & Fasman beta-sheet prediction
  - Chou & Fasman beta-turn prediction
- Flexibility
  - Karplus & Schulz flexibility prediction
    - 3 separate scales
- Surface exposure
  - Emini surface accessibility prediction
    - Emini equation
- Antigenicity
  - Kolaskar & Tongaonkar antigenicity prediction
    - Kolaskar prediction method



1. Specify protein sequence

2. Select a method

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

Antibody Epitope Prediction Result - Mozilla Firefox

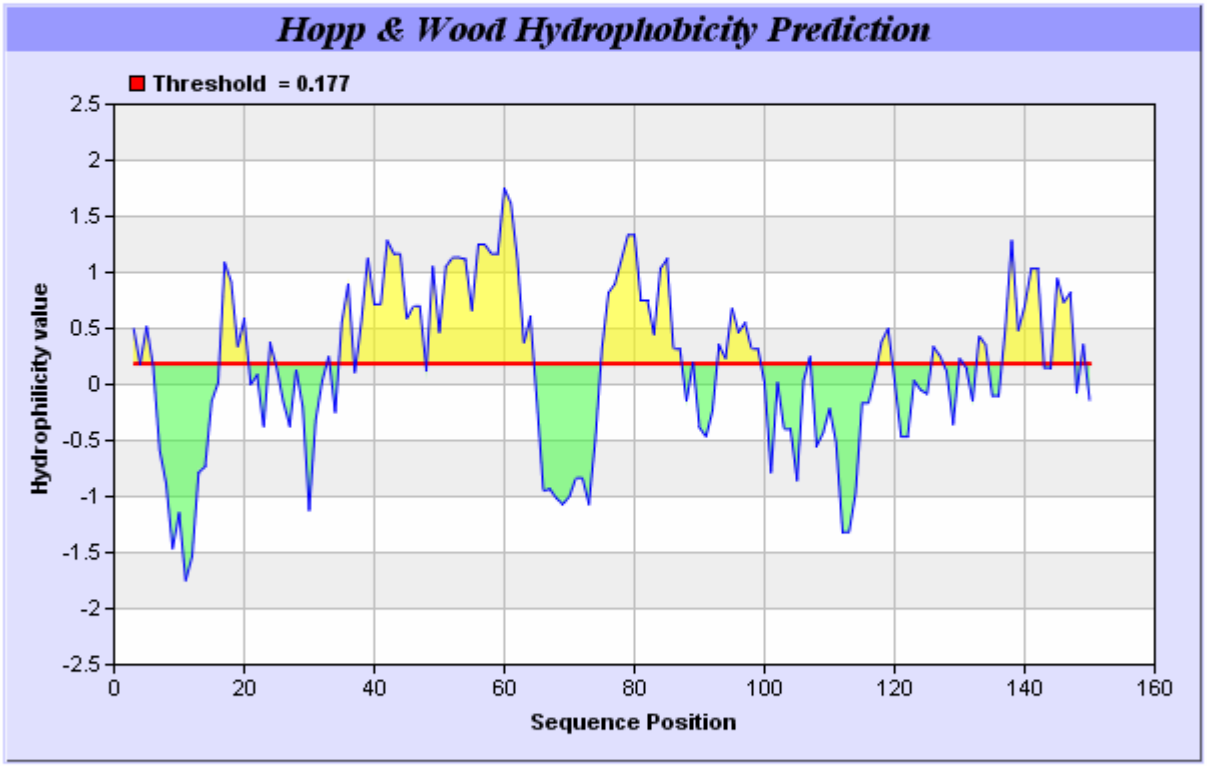
File Edit View Go Bookmarks Tools Help

Hopp & Wood Hydrophobicity Prediction

Sequence:

```
  1 VLSEGEWQLV LHVWAKVEAD VAGHGQDILI RLFKSHPETL EKFDRFKHLK TEAEMKASED
 61 LKKHGVTVLT ALGAILKKKG HHEAELKPLA QSHATKHKIP IKYLEFISEA IIHVLHSRHP
121 GNFGADAGGA MNKALELFRK DIAAKYKELG YQG
```

Center position: 3 **Window size:** 6 Re-Caculate



Average: 0.177 **Minimum:** -1.750 **Maximum:** 1.750 **Threshold:** 0.177 Change

Click here to view plotted values in table format

Reference: Hopp TP & Woods KR. Prediction of protein antigenic determinants from amino acid sequences. Proc Natl Acad Sci U S A. 1981 Jun;78(6):3824-8.

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

B-cell epitope identification

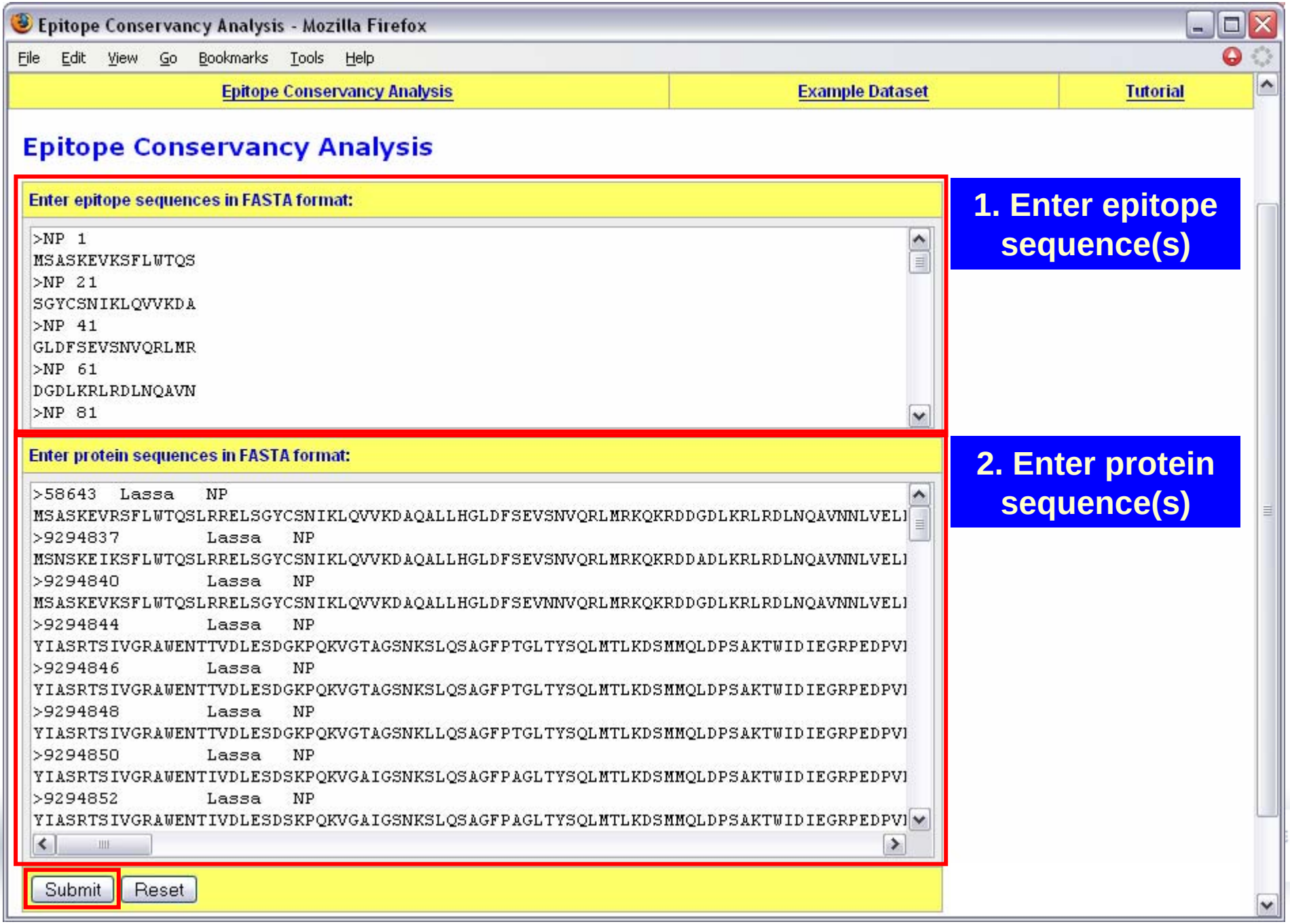
- Tool evaluation
  - B-cell epitope prediction workshop
- New tool development (2nd release)
  - Sequence-based approach
    - Linear epitopes
  - Structure-based approach
    - Linear + conformational epitopes

Outline

- Tool integration
- T cell epitope identification tools
- B cell epitope identification tools
- Epitope analysis tools
- Visualization tools

Epitope Analysis I: Conservancy

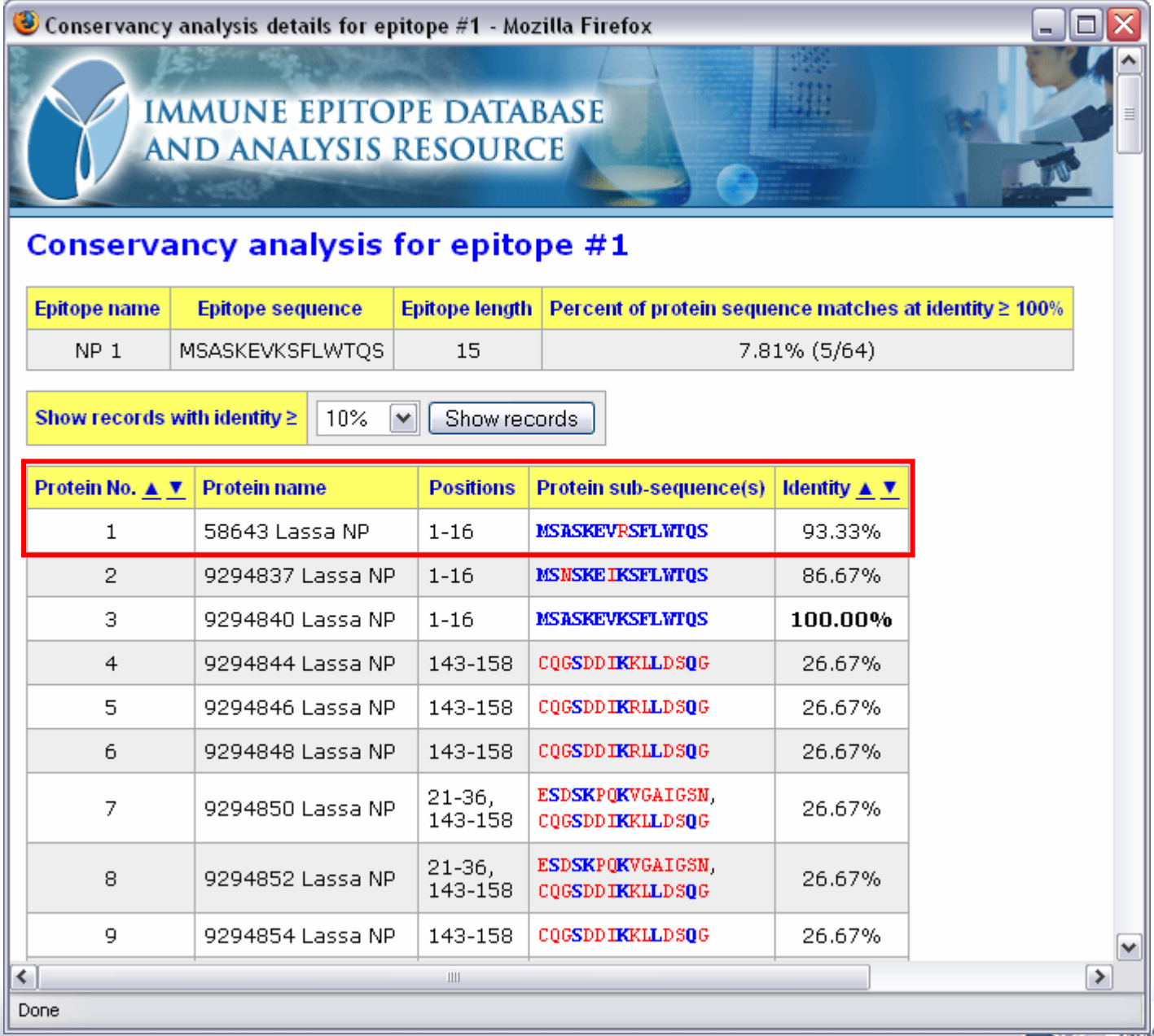
- How well is an epitope conserved across different sources (e.g. viral strains)?


Epitope Conservancy Analysis - Mozilla Firefox
File Edit View Go Bookmarks Tools Help
Epitope Conservancy Analysis
Example Dataset
Tutorial
Epitope Conservancy Analysis
Enter epitope sequences in FASTA format:
>NP 1
MSASKEVKSFLWTQS
>NP 21
SGYCSNIKLQVVKDA
>NP 41
GLDFSEVSNVQRLMR
>NP 61
DGDLKRLRDLNQAVN
>NP 81
Enter protein sequences in FASTA format:
>58643 Lassa NP
MSASKEVRSFLWTQSLRRELSGYCSNIKLQVVKDAQALLHGLDFSEVSNVQRLMRKQKRDDGDLKRLRDLNQAVNNLVELI
>9294837 Lassa NP
MSNSKEIKSFLWTQSLRRELSGYCSNIKLQVVKDAQALLHGLDFSEVSNVQRLMRKQKRDDADLKRLRDLNQAVNNLVELI
>9294840 Lassa NP
MSASKEVKSFLWTQSLRRELSGYCSNIKLQVVKDAQALLHGLDFSEVNNVQRLMRKQKRDDGDLKRLRDLNQAVNNLVELI
>9294844 Lassa NP
YIASRTSIVGRAWENTTVDLESDGKPQKVGTAGSNKSLQSAGFPTGLTYSQLMTLKDSMMQLDPSAKTWIDIEGRPEDPVI
>9294846 Lassa NP
YIASRTSIVGRAWENTTVDLESDGKPQKVGTAGSNKSLQSAGFPTGLTYSQLMTLKDSMMQLDPSAKTWIDIEGRPEDPVI
>9294848 Lassa NP
YIASRTSIVGRAWENTTVDLESDGKPQKVGTAGSNKLLQSAGFPTGLTYSQLMTLKDSMMQLDPSAKTWIDIEGRPEDPVI
>9294850 Lassa NP
YIASRTSIVGRAWENTIVDLESDSKPQKVGAIGSNKSLQSAGFPAGLTYSQLMTLKDSMMQLDPSAKTWIDIEGRPEDPVI
>9294852 Lassa NP
YIASRTSIVGRAWENTIVDLESDSKPQKVGAIGSNKSLQSAGFPAGLTYSQLMTLKDSMMQLDPSAKTWIDIEGRPEDPVI
Submit
Reset
1. Enter epitope sequence(s)
2. Enter protein sequence(s)

Epitope Conservancy Analysis Result

Minimum identity threshold: 100% Set

Epitope No. ▲ ▼	Epitope name	Epitope sequence	Epitope length	Percent of protein sequence matches at identity ≥ 100% ▲ ▼	Minimum identity	Maximum identity ▲ ▼	View details
1	NP 1	MSASKEVKSFLWTQS	15	7.81% (5/64)	20.00%	100.00%	Go
2	NP 21	SGYCSNIKLQVVKDA	15	17.19% (11/64)	26.67%	100.00%	Go
3	NP 41	GLDFSEVSNVQRLMR	15	15.62% (10/64)	26.67%	100.00%	Go
4	NP 61	DGDLKRLRDLNQAVN	15	4.69% (3/64)	20.00%	100.00%	Go
5	NP 81	KSTQQKSVLRVGTLS	15	3.12% (2/64)	26.67%	100.00%	Go
6	NP 101	TLAADLEKLKSKVIR	15	6.25% (4/64)	33.33%	100.00%	Go
7	NP 121	SSGVYMGNLSSQQLD	15	6.25% (4/64)	33.33%	100.00%	Go
8	NP 141	LNMIGMSGGNQGAQT	15	3.12% (2/64)	26.67%	100.00%	Go
9	NP 161	VRVWDVKNAELLNNQ	15	10.94% (7/64)	20.00%	100.00%	Go
10	NP 181	SLTLACLTKQGQVDL	15	17.19% (11/64)	26.67%	100.00%	Go
11	NP 201	ALTDLGLIYTAKYPN	15	17.19% (11/64)	26.67%	100.00%	Go
12	NP 221	RLTQSHPILNMIDTK	15	7.81% (5/64)	20.00%	100.00%	Go
13	NP 241	ISGYNFSLGAAVKAG	15	15.62% (10/64)	26.67%	100.00%	Go
14	NP 261	GGNMLETIKVSPQTM	15	10.94% (7/64)	26.67%	100.00%	Go
15	NP 281	SILKVKKSLGMFISD	15	0.00% (0/64)	26.67%	93.33%	Go
16	NP 301	NPYENILYKICLSGD	15	14.06% (9/64)	20.00%	100.00%	Go
17	NP 321	ASRTSITGRAWENTV	15	67.19% (43/64)	86.67%	100.00%	Go
18	NP 341	DGKPQKAGSNNSNKS	15	28.12% (18/64)	60.00%	100.00%	Go



Blue: Matching residues

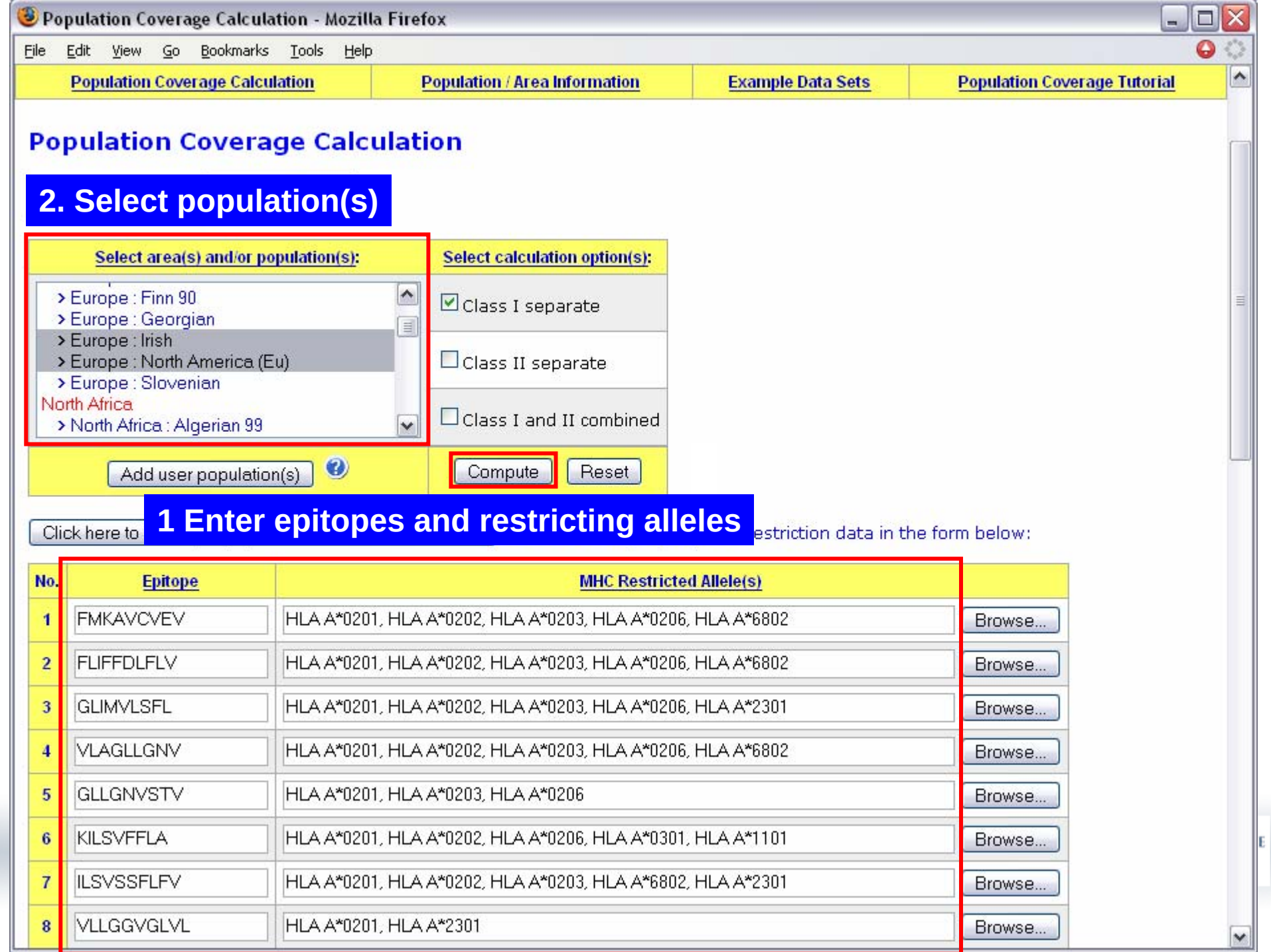
Red: Non-matching residues

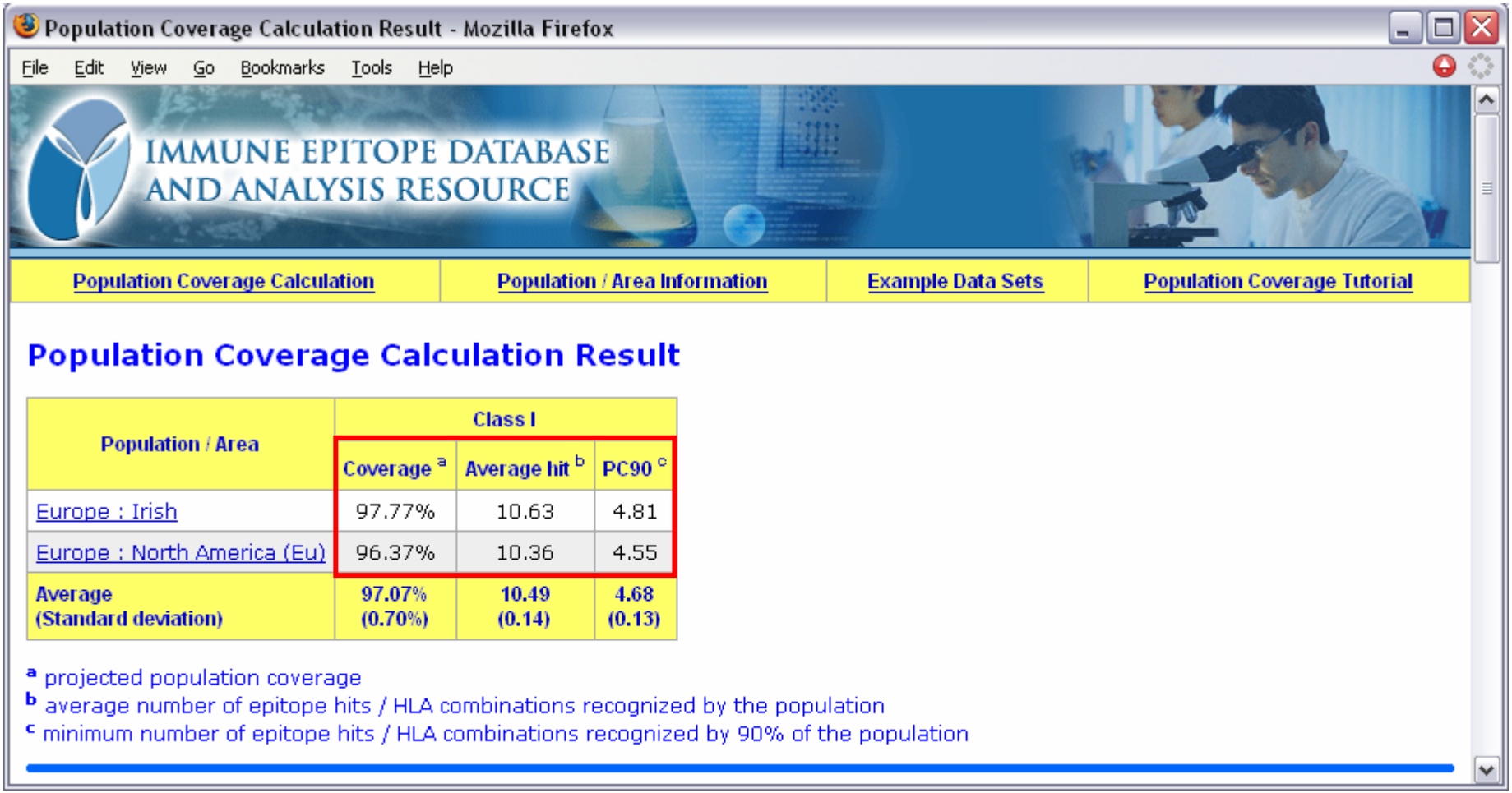
Epitope Analysis II: Population Coverage

- Given a set of epitopes with known MHC restriction(s), what is the predicted coverage in a population with known MHC allele frequencies?

Background

- MHC restriction
  - T cell epitope will elicit a response only in individuals that express an MHC molecule capable of binding that particular epitope
- MHC polymorphism
  - Over a thousand different MHC alleles are known in humans
  - MHC alleles are found at dramatically different frequencies in different ethnicities
- Motivation
  - How to design T-cell epitope-based diagnostics and vaccines to be effective across different populations


Population Coverage Calculation - Mozilla Firefox
File Edit View Go Bookmarks Tools Help
Population Coverage Calculation
Population / Area Information
Example Data Sets
Population Coverage Tutorial
Population Coverage Calculation
2. Select population(s)
Select area(s) and/or population(s):
> Europe : Finn 90
> Europe : Georgian
> Europe : Irish
> Europe : North America (Eu)
> Europe : Slovenian
North Africa
> North Africa : Algerian 99
Select calculation option(s):
Class I separate
Class II separate
Class I and II combined
Add user population(s)
Compute
Reset
1 Enter epitopes and restricting alleles
Click here to
estriction data in the form below:
No.
Epitope
MHC Restricted Allele(s)
1 FMKAVCVEV HLA A*0201, HLA A*0202, HLA A*0203, HLA A*0206, HLA A*6802 Browse...
2 FLIFFDLFLV HLA A*0201, HLA A*0202, HLA A*0203, HLA A*0206, HLA A*6802 Browse...
3 GLIMVLSFL HLA A*0201, HLA A*0202, HLA A*0203, HLA A*0206, HLA A*2301 Browse...
4 VLAGLLGNV HLA A*0201, HLA A*0202, HLA A*0203, HLA A*0206, HLA A*6802 Browse...
5 GLLGNVSTV HLA A*0201, HLA A*0203, HLA A*0206 Browse...
6 KILSVFFLA HLA A*0201, HLA A*0202, HLA A*0206, HLA A*0301, HLA A*1101 Browse...
7 ILSVSSFLFV HLA A*0201, HLA A*0202, HLA A*0203, HLA A*6802, HLA A*2301 Browse...
8 VLLGGVGLVL HLA A*0201, HLA A*2301 Browse...



Coverage: Projected population coverage

Average hit: Average number of epitope hits / HLA combinations recognized in the population

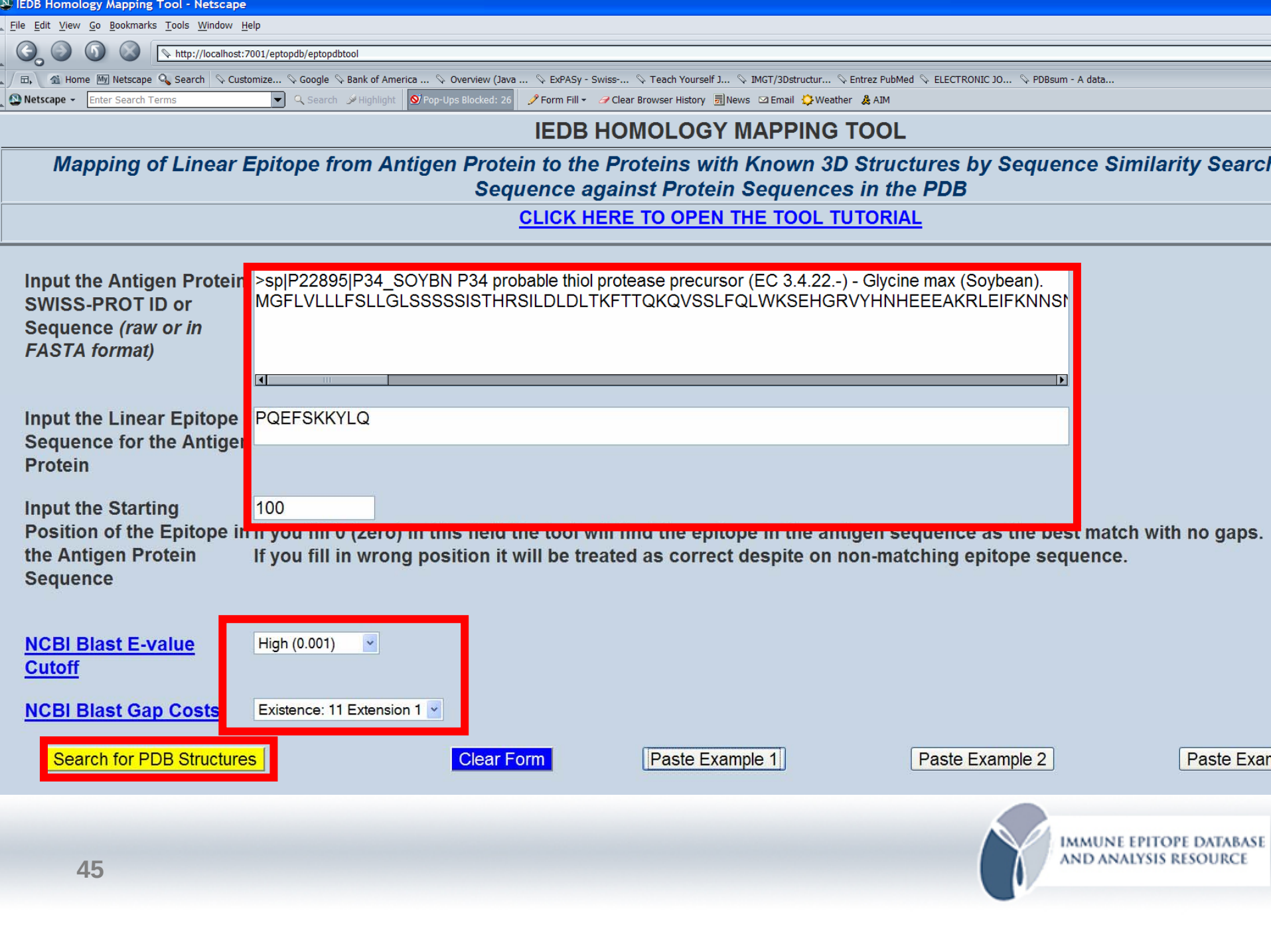
PC90: Minimum number of epitope hits / HLA combinations recognized by 90% of the population

Outline

- Tool integration
- T cell epitope identification tools
- B cell epitope identification tools
- Epitope analysis tools
- Visualization tools

Visualization Tools

- **Epitope Viewer**
  Displays 3D structure and contact information curated in the IEDB
- **Homology Mapping Tool**
  Maps linear epitopes to proteins with known 3D structure from the Protein Data Bank (PDB)



IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

List of PDB IDs related to the epitope PQEFSKKYLQ at position 100 in the query antigen sequence

PDB ID	Chain	Alignment	Alignment Length (including gaps)	Sequence Identity in the Alignment (including gaps) (%)	E Value	Number of Gaps in the Alignment	Query Epitope Sequence Identity in the Alignment (%)
1PCI	C	QUERY 35 TTQKQVSSLFQLWKSEHGRVYHNHEEEAKRLEIFKNNSNYIRDMNANRKSPHSHRLGLN 1PCI_C 13 TSTERLIQLFNSWMLNHNKFYENVDEKLYRFEIFKDNLNYIDETN---KKNNSYWLGLN ADITPQEFSKKYLQAPKDVSQQIKMANK ADLSNDEFNEKYVGSLIDATIEQSYDEK QUERY 215 IATDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISV 1PCI_C 186 IHLRSKYPYKAKQGTCRAKQ------VGGPIVKTSGVGRVQPNNEGNLLNAIAKQPVSV QUERY 275 IDAK--DFHLYTGGIYDGENCTSPYGINHFVLLVGYGSADGVDYWIAKNSWGFDWGEDG 1PCI_C 240 VESKGRPFQLYKGGIFEGPCGTK---VDGAVTAVGYGKSGGKGYILIKNSWGTAWGEKG QUERY 333 IWIQRNTGNLLGVCGMNYFASYPTK 1PCI_C 297 IRIKRAPGNSPGVCGLYKSSYYPTK	325	37.0	6.60854e-50	18	40.0 (4/10)
1PCI	B	QUERY 35 TTQKQVSSLFQLWKSEHGRVYHNHEEEAKRLEIFKNNSNYIRDMNANRKSPHSHRLGLNK 1PCI_B 13 TSTERLIQLFNSWMLNHNKFYENVDEKLYRFEIFKDNLNYIDETN---KKNNSYWLGLNE QUERY 95 FADITPQEFSKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQG	325	37.0	6.60854e-50	18	40.0 (4/10)

Display in Epitope Viewer


MBT EpitopeViewer: 1pci
Full Sequences
Debug
Antigen (C):
LTSTERLIQLFNSWMLNHNKFYENVDEKLYRFEIFKDNLNYIDETNKKNNSYWLGLNEFADLSNDEFNEKYVGSLIDATI
EQSYDEEFINEDIVNLPENVDWRKKGAVTPVRHQGSCGSCWAFSAVATVEGINKIRTGKLVELSEQELVDCERRSHGCKG
GYPPYALEYVAKNGIHLRSKYPYKAKQGTCRAKQVGGPIVKTSGVGRVQPNNEGNLLNAIAKQPVSVVVESKGRPFQLYK
GGIFEGPCGTKVDGAVTAVGYGKSGGKGYILIKNSWGTAWGEKGYIRIKRAPGNSPGVCGLYKSSYYPTKN
Structure
Click here to go to the PDB (1pci)
Options
Display contacting atoms for...
Antigen
Label:
by residues
by atoms
Reset
Save 3d image
Help
Tutorial
Credits
John Beaver, et al.

Acknowledgments

- LIAI
  - **A. Sette**
  - **H. Bui**
  - **J. Mokili**
  - **S. Wilson**
  - **W. Fleri**
  - **M. Sathiamurthy**
  - **H. Grey**
  - **J. Sidney**
  - **N. Salimi**
  - **G. Moore**
  - **L. Zerebsky**
  - **R. Chen**
  - **R. Vita**
  - **M. Alexander**
- SAIC
  - **S. Stewart**
  - **D. di Ferdinando**
  - **P. Surko**
  - **S. Way**
  - **T. Carolan**
- SDSC
  - **P. Bourne**
  - **J. Pomarenko**
  - **J. Beaver**
  - **K. Addess**
- NIAID
- OTHERS
  - **V. Brusic**
  - **W. Hildebrand**
  - **S. Buus**
  - **Large Scale Epitope Groups**
  - **Immunological Databases**

Points of Interaction with BRCs

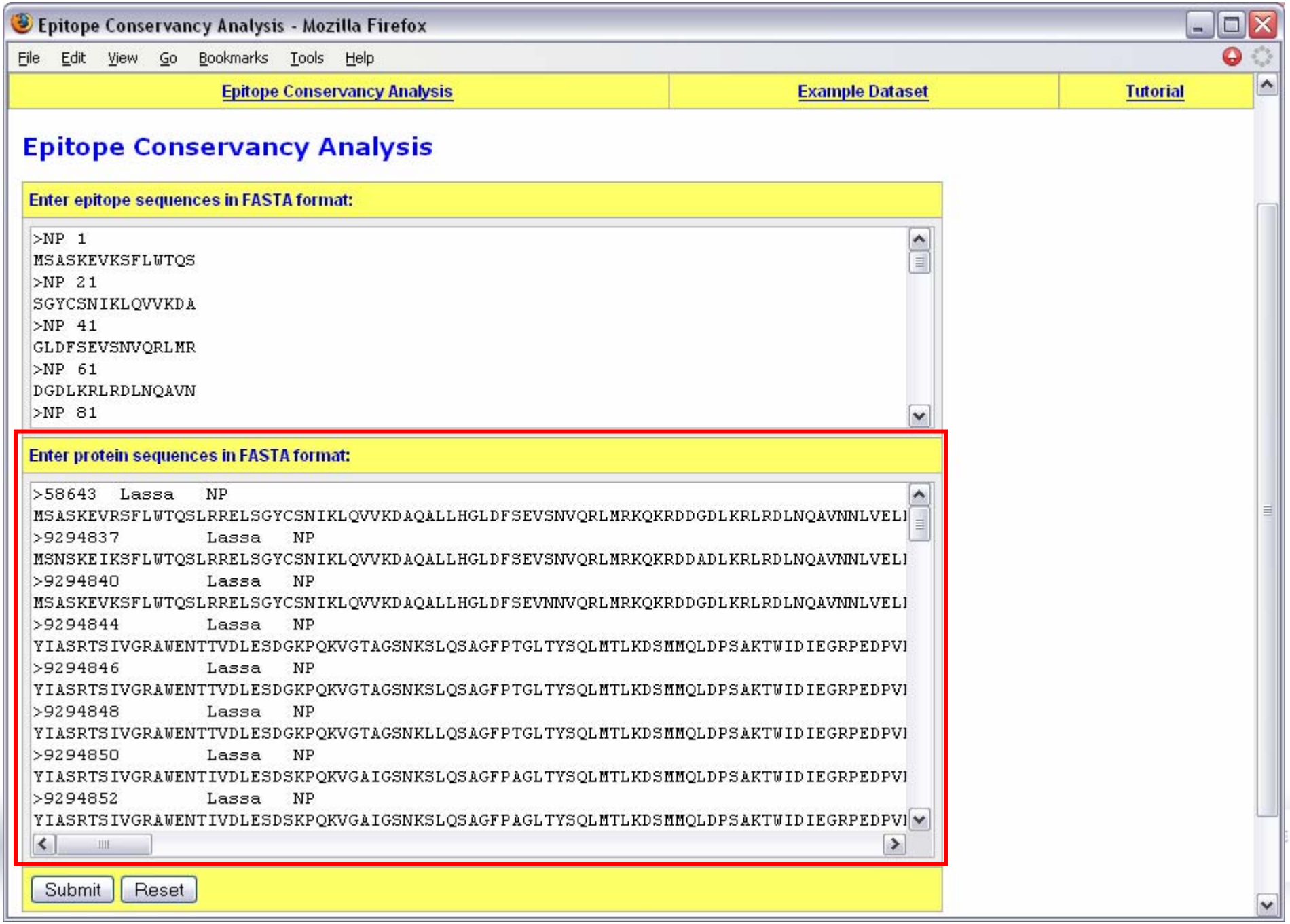
- Assigning source proteins to epitopes
- Tools
  - Epitope Conservancy
  - Direct linking
- Direct links to pathogen specific information
- Point out literature missed

Assigning Epitope Sources

- Literature: "... Epitope SLRTYKWQL comprising residues 46-54 of the influenza matrix protein..."
- Problem: We often want sequence of source protein
- Process: assign a SwissProt / GenBank protein that:
  - contains epitope (position match if possible)
  - matches source species (strain if possible)
  - matches name
- Better: Non-redundant set of high quality sequences with pathogen specific consistent naming conventions

Points of Interaction with BRCs

- Assigning source proteins to epitopes
- Tools
  - Epitope Conservancy
  - Direct linking
- Direct links to pathogen specific information
- Point out literature missed


Epitope Conservancy Analysis - Mozilla Firefox
File Edit View Go Bookmarks Tools Help
Epitope Conservancy Analysis
Example Dataset
Tutorial
Epitope Conservancy Analysis
Enter epitope sequences in FASTA format:
>NP 1
MSASKEVKSFLWTQS
>NP 21
SGYCSNIKLQVVKDA
>NP 41
GLDFSEVSNVQRLMR
>NP 61
DGDLKRLRDLNQAVN
>NP 81
Enter protein sequences in FASTA format:
>58643 Lassa NP
MSASKEVRSFLWTQSLRRELSGYCSNIKLQVVKDAQALLHGLDFSEVSNVQRLMRKQKRDDGDLKRLRDLNQAVNNLVELI
>9294837 Lassa NP
MSNSKEIKSFLWTQSLRRELSGYCSNIKLQVVKDAQALLHGLDFSEVSNVQRLMRKQKRDDADLKRLRDLNQAVNNLVELI
>9294840 Lassa NP
MSASKEVKSFLWTQSLRRELSGYCSNIKLQVVKDAQALLHGLDFSEVNNVQRLMRKQKRDDGDLKRLRDLNQAVNNLVELI
>9294844 Lassa NP
YIASRTSIVGRAWENTTVDLESDGKPQKVGTAGSNKSLQSAGFPTGLTYSQLMTLKDSMMQLDPSAKTWIDIEGRPEDPVI
>9294846 Lassa NP
YIASRTSIVGRAWENTTVDLESDGKPQKVGTAGSNKSLQSAGFPTGLTYSQLMTLKDSMMQLDPSAKTWIDIEGRPEDPVI
>9294848 Lassa NP
YIASRTSIVGRAWENTTVDLESDGKPQKVGTAGSNKLLQSAGFPTGLTYSQLMTLKDSMMQLDPSAKTWIDIEGRPEDPVI
>9294850 Lassa NP
YIASRTSIVGRAWENTIVDLESDSKPQKVGAIGSNKSLQSAGFPAGLTYSQLMTLKDSMMQLDPSAKTWIDIEGRPEDPVI
>9294852 Lassa NP
YIASRTSIVGRAWENTIVDLESDSKPQKVGAIGSNKSLQSAGFPAGLTYSQLMTLKDSMMQLDPSAKTWIDIEGRPEDPVI
Submit
Reset

Points of Interaction with BRCs

- Assigning source proteins to epitopes
- Tools
  - Epitope Conservancy
  - Direct linking
- Direct links to pathogen specific information
- Point out literature missed

Immune Epitope Database and Analysis Resource - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

Display Settings:

Format: Summary

Show: 10

Options:

[New Query]
[Revise Query]
[Save Query]
[View Query Details]
[Define Custom Report]

Analyze Selected Records:

Tool: T Cell Epitope Prediction

Analyze

BRC ←→IEDB

9 items found, displaying all items.
Page **1**

	Links	Reference	Structure	Source	Assay
☑	Details	Samita S Andreansky Journal of virology. 2005	RTFSFQLI	Influenza A virus (A/PR/8/34(H1N1)) NS2	T + Cytokine Release-IFN-g
☐	Details	Samita S Andreansky Journal of virology. 2005	LSLRNPILV	Influenza A virus (A/PR/8/34(H1N1)) PB1-F2	T + Cytokine Release-IFN-g
☐		(Baltimore, Md. : 1950) 2005			Release-IFN-g

```
<form action="http:/immuneepitope.org/tools/mhc_I_binding"
    method="post">
    <input name="sequence" value="RTFSFQLI" />
    <input type="submit" />
</form>
```

9 items found, displaying all items.
Page **1**

Export all results: Excel

Help us make the IEDB better by reporting erroneous entries

Much of the information contained in the IEDB is manually extracted by experts from scientific literature using significant effort to ensure accuracy. If you recognize an error or misinterpretation, we would greatly appreciate your help by using the feedback form to report any potential problems you observe. Please be sure to include (1) the IEDB identifier of the problematic record, (2) the field name(s) in which the problem is located, and (3) the corrected field values

Points of Interaction with BRCs

- Assigning source proteins to epitopes
- Tools
  - Epitope Conservancy
  - Direct linking
- Direct links to pathogen specific information
- Point out literature missed

Immune Epitope Database and Analysis Resource - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

Display Settings:

Format: Summary

Show: 10

Options:

[New Query]
[Revise Query]
[Save Query]
[View Query Details]
[Define Custom Report]

Analyze Selected Records:

Tool: T Cell Epitope Prediction

Analyze

9 items found, displaying all items.
Page **1**

	Links	Reference	Structure	Source	Assay
☑	Details	Samita S Andreansky Journal of virology. 2005	RTFSFQLI	Influenza A virus (A/PR/8/34(H1N1)) NS2	T + Cytokine Release-IFN-g
☐	Details	Samita S Andreansky Journal of virology. 2005	LSLRNPILV	Influenza A virus (A/PR/8/34(H1N1)) PB1-F2	T + Cytokine Release-IFN-g
☑	Details	David H Canaday Journal of immunological methods. 2003	GLKGGPSTE	Influenza A virus (A/PR/8/34(H1N1)) Matrix protein 2	T + Cytokine Release-IFN-g
☑	Details	S M Mansour Haeryfar Journal of immunology (Baltimore, Md. : 1950) 2005	SSLENFRAYV	Influenza A virus (A/Puerto Rico/8/34(H1N1)) Polymerase acidic protein (PA)	T + Cytokine Release-IFN-g
☑	Details	S M Mansour Haeryfar Journal of immunology (Baltimore, Md. : 1950) 2005	ASNENMETM	Influenza A virus (A/Puerto Rico/8/34(H1N1)) Nucleoprotein	T + Cytokine Release-IFN-g
☑	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	LYQNVGTYV	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☐	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	IYATVAGSL	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☐	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	TYVSVGTST	Influenza A virus (A/Japan/305/57(H2N2)) Hemagglutinin precursor	T + Cytokine Release-IFN-g
☑	Details	Christopher W Lawrence Journal of immunology (Baltimore, Md. : 1950) 2005	TYQRTRALV	Influenza A virus (A/Japan/305/57(H2N2)) Nucleoprotein	T + Cytokine Release-IFN-g

9 items found, displaying all items.
Page **1**

Export all results: Excel

Help us make the IEDB better by reporting erroneous entries

Much of the information contained in the IEDB is manually extracted by experts from scientific literature using significant effort to ensure accuracy. If you recognize an error or misinterpretation, we would greatly appreciate your help by using the feedback form to report any potential problems you observe. Please be sure to include (1) the IEDB identifier of the problematic record, (2) the field name(s) in which the problem is located, and (3) the corrected field values

Points of Interaction with BRCs

- Assigning source proteins to epitopes
- Tools
  - Epitope Conservancy
  - Direct linking
- Direct links to pathogen specific information
- Point out literature missed